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(c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wistow G., Berstein S.L., Ray S., Wyatt M.K., Behal A., Touchman J.W., Bouffard G., Smith D., Peterson K.;

Experior Steroid-Exponse factors and similarities with retinal pigment epithelium.;

Mol. Vision 8:185-195(2002).

EMBL, AR033613, BAB18903.1;

EMBL, AR131616, AAK38840.1;

EMBL, AR33584; AAK38840.1;

EMBL, AR33584; AAK38840.1;

EMBL, AR335817; AAK2081.1;

EMBL, AF33517; AAK2081.1;

EMBL, AC7591; JG7591.
                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Spinal cord-derived growth factor-B (MSTP036) (Platelet-derived growth factor D) (Iris expressed growth factor long form).
Name-bSCDGF-B; Synonyms=IEGF, PDGFD;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vernet C.,
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PubMed=1131881; DOI=10.1038/35074588;
PubMed=1131881; DOI=10.1038/35074588;
Alitalo K., Eriksson U.;
"PDGF-D is a specific, protease-activated ligand for the PDGF beta-
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=21092670; PubMed=11162582; DOI=10.1006/bbrc.2000.4187;
MEDLINE=21092670; R., Imaki J., Miyata Y.;
"Molecular cloning of SCGF-B, a novel growth factor homologous to SCDGF/PDGF-C/fallotein.";
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MEDLINE=21231309, PubMed=11331882; DOI=10.1038/35074593;
LaRochelle W.J., Jeffers M., McDonald W.F., Chillakuru R.A.,
Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet
Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets J.,
Shimkets R.A., Rothberg J.M., Lichenstein H.S.;
"PDGF D, A Novel Procease-Activated Growth Factor.";
Nat. Cell Biol. 3:517-521(2001).
                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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GO; GO:0008083; F:growth factor activity; IEA.
GO; GO:0008083; F:growth factor activity; IEA.
GO; GO:0008151; P:cell growth and/or maintenance; IEA.
InterPro; IPR000859; CUB.
InterPro; IPR010916; TONB_Box_N.
Formar; PF00431; CUB; 1.
SMART; SM00042; CUB; 1.
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                                             370 AA.
                                            PRT;
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Nat. Cell Biol. 3:512-516(2001).
                                             PRELIMINARY;
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Wistow G., Berstein S.L., Ray S., Wyatt M.K., Behal A., Touchman J.W.,
Wistow G., Smith D., Peterson K.;
"Expressed sequence tag analysis of adult human iris for the NEIBank
Project: steroid-response factors and similarities with retinal
pigment epithelium."
Mol. Vision 8:185-195(2002).
                                                                                                                                                                                   1 MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDESNHLTDLYRRDETIQVKG
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
25-OCT-2004 (TrEMBLrel. 17, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
1ris-expressed growth factor short form (Platelet derived growth factor D, isoform 2) (SCDGF-B).
Name=IEGF; Synonyms=PDGFD; ORFNames=UNQ1899;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PS01180; CUB; 1.
PS50278; PDGF 2; 1.
PS00430; TONB_DEPNDENT REC 1; UNKNOWN 1.
370 AA; 42848 MW; D387F485E7BB7674 CRC64;
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TISSUE=Iris;
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SEQUENCE
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282 ANVVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTM 341
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae, Rattus.
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MEDLINE=21032670; PubMed=11162582; DOI=10.1006/bbrc.2000.4187;

Hamada T., Ui-Tei K., Imaki J., Miyata Y.;

Hondeular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-C/fallotein.";

Biochem. Biophys. Res. Commun. 280:733-737(2001).

EMBL; AB052170; BB1818920.1; -.

HSSP; Q9UCV4; 1NZI.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
1ris-expressed growth factor (Fragment).
Name=PDGFD;
Name=PDGFD;
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ray S., Wistow G.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
BMBL, AY347260, AAQ24382.1;
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0008151; P:growth factor activity; IEA.
R GO; GO:0008151; P:growth factor activity; IEA.
R InterPro; IPR0000559; CUB.
R InterPro; IPR0000559; CUB.
R SMART; SW000421; CUB; 1.
R PROSITE; PS01180; CUB; 1.
R PROSITE; PS01180; CUB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34616 MW; 716C873C9C01C0C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0016020; C:membrane; IEA.
GO; GO:0008083; F:growth factor activity; IEA.
GO; GO:0008151; P:cell growth and/or maintenance; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9EQT1;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35; DB 2; Lo
Pred. No. 2.8e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 YRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVN 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 YRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVN 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. wc.
                                                                                                                                                  342 ALVDIOLDHHERCDCICSSRPPR 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                    348 ALVDIQLDHHERCDCICSSRPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=rSCDGF-B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                               Q6V9H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9EQT1
                                                                                                                                                                                                                                                                                                                            RESULT 3
                                                                                                                                                                                                                                                                                                                                                                 Q6V9H4
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Genome Res. 13:2265-2270(2003).

EMBL; AY027518; AAR20082.1; -...

EMBL; AY027518; AAR30645.1; -...

REMBL; AY359116; AAQ89474.1; -...

REMBL; AY359116; AAQ89474.1; -...

R HSSP; Q94789; INTO.

GO; G0:0016020; C:membrane; IEA.

GO; G0:0016020; C:membrane; IEA.

GO; G0:00160151; F:cell growth factor activity; IEA.

R InterPro; IPR000072; PD growth factor.

R InterPro; IPR000072; PD growth factor.

R InterPro; IPR010916; TONB_Box_N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 ANVVFEPRCLLVQRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTM 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 NPESWQEDLENMYLDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKL 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 SLLEDFQPAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYF 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NPESWQEDLENMYLDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKL 287
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhitling M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chow B., Chui C., Crowley C., Currell B., Douel B., Dowd Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Laton D., Foster J., Kilmowski L., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A. Vandlen R., Watanabe C., Weand D., Woods K., Xie M.H., Yansura D. Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS01180; CUB; 1.
PROSITE; PS01278; PDGF 2; 1.
PROSITE; PS00430; TONB DEPENDENT REC 1; UNKNOWN 1.
SEQUENCE 364 AA; 42166 MW; 245C53EBDDEA9EAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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Best Local S:
Matches 323
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SEQUENCE FROM N.A.

STRAIN=FVB/N, TISSUE=Mammary tumor;

MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Alschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhar N.K.,

A Dischel S.F., Jordan H., Moore T., Max S.I., Wang J., Haith F.,

A Dischelor D.M., Hong L.,

B Dischelor D.M., Hong L.,

B Dischelor D.M., Hong L.,

B Eromstein M.J., Usdin T.B., Toochiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Brownstein M.J., Usdin T.B., Toochiyuki S., Carninci P., Prange C.,

R Raha S.S., McEwan P.J., McKernan R.J., Marke J.A., Gunzaren P.H.,

A Bask S.A., McEwan P.J., McKernan R.J., Marke J.A., Gunzaren P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcerfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Sochein J.E.,

T "Generation and initial analysis of more than 15,000 full-length human man and mouse chan a control of the control o
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MGD; MG1:1919035; Pdgfd.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:005573; Pregulation of peptidyl-tyrosine phosphoryla. . .; IDA.
InterPro; IPR000859; CUB.
SMART; SM00421; CUB, 1.
PROSITE; PS01180; CUB; 1.
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                      Length 370;
                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC030896; AAH30896.1; -.
                InterPro; IPR000072; PD_growth_factor.

Pfam; PP00431, CUB; 1.

SMART; SM00042; CUB; 1.

SMART; SM00141; PDGF; 1.

PROSITE; PS01180; CUB; 1.

PROSITE; PS0278; PDGF 2; 1.

SEQUENCE 370 AA; PGF 2; 1.
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; 30228 MW; 2EEC3F6373A52D09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                 8.6%; Score 32; DB 2; Le
100.0%; Pred. No. 4.4e-24;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                  ATPQSASIKALRNANLRRDESNHLTDLYRRDE 54
                                                                                                                                                                                                                                                                                             23 ATPOSASIKALRNANLRRDESNHLTDLYRRDE 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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STRAIN=FVB/N; TISSUE=Mammary tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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InterPro; IPR000859; CUB
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01-OCT-2003 (TrEMBLrel.
Pdgfd protein.
                                                                                                                                                                                                                    Local Similarity
nes 32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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DB 2; Length 261; 5.1e-19;

Score 27; Pred. No.

7.3%; S 100.0%;

Query Match Best Local Similarity

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=whole body;
MEDLINE=20499374; PubMed-11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs."; Nature 420:563-573 (2002).
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:
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    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=DALB/C;
MEDLINE=DALB/C;
MEDLINE=21211380; PubMed=11331882; DOI=10.1038/35074593;
LaRochelle W.J., Geffers M., McDonald W.F., Chillakuru R.A.,
Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets J.,
Shimkets R.A., Rothberg J.M., Lichenstein H.S.;
"PDGF D., A Novel Protesse-Activated Growth Factor.";
                                                                                                                                                                                                                                               05-JUL-2004 (TERMBLrel 27, Last annotation update)
Platelet-derived growth factor D (Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110003109 product:platelet-derived growth factor D).
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                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metaria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090;
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Indels
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STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=2108560; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
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0
                                                                                                                                                                                                                                       Last sequence update)
                                                                                                                                                                               370 AA
Mismatches
                                       142 SRTNQIKITFKSDDYFVAKPGFKIYYS 168
                                                             142 SRTNOIKITFKSDDYFVAKPGFKIYYS
                                                                                                                                                                                           092517; 09D1L8;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Whole body;
The FANTOM Consortium,
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  Conservative
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es 9, Conservative
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TISSUE=Seeds;
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05-JUL-2004
05-JUL-2004
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Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiracka T., Hori F.,

I motani K., Ishii Y., Itoh M., Hiramoto K., Kasukawa T., Kato H.,

Kawai J., Kojima Y., Konono H., Kouda M., Koya S., Kurihara C.,

A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

A Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

A Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

Muramatsu M., Hayashizaki Y.;

L Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

E EMBL; AK003359; BAB22735.2; -.

R EMBL; AK003359; DABZ2735.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                      MOD; MGT:1919035; Pdgfd.
MOD; MGT:1919035; Pdgfd.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005013; CUB; D: regulation of peptidyl-tyrosine phosphoryla. . .; IDA.
Pfam; PF00431; CUB; 1.
SMART; SM0044; PDGF, 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS0278; PDGF, 2; 1.
SEQUENCE 370 AA; 42809 MW; 9E80B4CF6813BFBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBIrel. 19, Last sequence update)
01-OCT-2003 (TrEMBIrel. 25, Last annotation update)
Metallothionein-like protein.
Metallothionein-like protein.
Guerus suber (Cork oak).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroaids I; Fagales; Fagaceae; Quercus.
NCBL_TaxID=58331;
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Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKRN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.3%; Score 27; DB 2; Length 370; 100.0%; Pred. No. 6.9e-19; ive 0; Mismatches 0; Indel8
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2.4%; Score 9; DB 2
Best Local Similarity 100.0%; Pred. No. 0.8
Mạtches 9; Conservative 0; Mismatches
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Pagus sylvatica (Beechnut).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids,
eurosids I; Fagales, Fagaceae, Fagus.
NCBI_TaxID=28930;
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Calvo A.P., Lorenza Co., Nicolas C., Nicolas G., Rodriguez D.;
AJ130886 from Fagus sylvatica L. seeds. (PGR99-073).";
Plant Physiol. 120:633-633(1999).
BMBL; AJ130886, CAA10222.1;
GO, GO.0046872; F:metal ion binding; IEA.
InterPro; IPR000347; Metallthion 15p.
ProDom; PD001611; Metallthion 15p, 1.
ProDom; PD001611; M773 MW; 69360779AF6D6C4A CRC64;
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                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Sun X., Xian X., Hong K., Kajiuchi T.;
Sun X., Xian X., Hong K., Kajiuchi T.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AB176565; BAD18383.1; -
GO; GO:0046872; F:metal ion binding; IEA.
InterPro; IPR000347; Metallthion_15p.
Prom; PP01439; Metallthion_2: 1.
Probom; PP01611; Metallthion 15p; 1.
SEQUENCE 77 AA; 7728 MW; 7D7911A020BD903C CRC64;
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Last sequence update)
Last annotation update)
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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100.0%; Pred. No. 0.88;
cive 0; Mismatches
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100.0%; Pred. No. 0.9;
ive 0; Mismatches
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                                                                                                                 NCBI_TaxID=3435;
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SEQUENCE
                                       Name=mt2;
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Best Local
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DDT READ DOWN DDR READ DDR READ DDR READ DDR PETT SQ
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                                             01-JAN'-1998 (TrEMBLrel. 05, Created)
01-JAN'-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Metallothionein-1 like protein.
Ocnanthe javanica (Water celery) (Water dropwort).
Bukaryora, Viridiplantes, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, endicotyledons, core eudicots, asterids, campanulids; Apiales; Apiaceae; Apioideae; Oenantheae; Oenanthe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukāryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
campanulids, Apiales, Apiaceae, Apioideae, apioid superclade,
Pimpinella clade, Pimpinella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                    DEPURABLE FACE.

Min B., Lee S.Y.;

Submitted (AUG-1997) to the EMBL/CenBank/DDBJ databases.

EMBL; AP017387; AAB70560.1; -.

GO; GO:0046872; F:metal ion binding; IEA.

InterPro; IFR000347; Metallothio_15p.

Pfam; PF01439; Metallothio_2; 1.

ProDom; PD001611; Metallthion 15p; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FACTOR TO THE STATE OF THE SERVICE BENEFIELD OF SUBMILTER (SEP-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, AF093585; AAC62510.1; --
EMBL, AF093585; AAC62510.1; --
EMBL, AF093585; AAC62510.1; --
InterPro; IPRO00347; Metallthion_15p.

Pfam; PF01439; Metallothio_2; 1.

ProDom; PD001611; Metallthion 15p; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Metallothionein-1-11ke protein.
Pimpinella brachycarpa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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                                       76 AA
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100.0%; Pred. No. 9.5
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.2%; Score 8; DB 2
100.0%; Pred. No. 9.5
[ve 0; Mismatches
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                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.20,
100.0%; PIC
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                     PRELIMINARY;
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                       022492
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Q9M4N0
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082581
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RESULT 10
                  022492
                                     ID DTT DDTT DDTT REP DR REP DR
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                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, magnoliids, Laurales, Lauraceae, Persea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protoplasts.
SIMILARITY: Belongs to the metallothionein superfamily. Family 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Vicia.
NCBL TaxID=3906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95036014; PubMed=7948889;
Foley R.C., Singh K.B.;
"Isolation of a Vicia faba metallothionein-like gene: expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
0
                                                                                                                                                                                                                                                                TISSUB-Fruit mesocarp;
Zamorano J.P., Evans A.D., Dopico B., Lowe A.L., Wilson I.D.,
Merodio C., Grierson D. the EMBL/GenBank/DDBJ databases.
Submitted (MAR.199) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ13145; CAB77242.1;
GO; GO:0046872; F:metal ion binding; IEA.
InterPro; IPR000347; Metallthion_15p.
Probom; PD001611; Metallthion_15p; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000347; Metallthion_15p.

Pfam; PF01439; Metallothio_2; 1.

ProDom; PD001611; Metallthion_15p; 1.

Metal-binding; Metal-thiolate cluster; Multigene family.

SEQUENCE 77 AA; 7730 MW; 7D7BADBD0223BF3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 AA; 7568 MW; A6433B2965E1566D CRC64;
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Metallothionein-like protein type 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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Pred. No. 9.5;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.2%; Scc...
100.0%; Pre
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                                                                                    Persea americana (Avocado)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 100.
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vicia faba (Broad bean).
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; asterids; lamids; Lamiales; Acanthaceae; Acanthaceae incertae sedis; Avicennia.
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                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=CLMT2;
Citrullus lanatus (Watermelon) (Citrullus vulgaris).
Eukaryophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyka; eudicotyledons; core eudicots; rosids;
eurosids I; Cucurbitales; Cucurbitaceae; Citrullus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Class I type 2 metallothionein.
Avicennia marina (Grey mangrove).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta.
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0
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                                                                                                                                                                                                                                           0; Indels
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                             SEQUENCE FROM N.A.
Schor T., Goldsbrough P.B., Adam Z., Tel-Or E.;
Schor T., Goldsbrough P.B., Adam Z., Tel-Or E.;
Submitted (1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF482470, AAL85416.1;
GO; GO: 6046872; F: metal ion binding; IEA.
InterPro; IPR000347; Wetallthion 15p.
Ftam; PF0149; Metallothio 2; 1.
SEQUENCE 77 AA; 7839 MW; 54DDF0CC032F50D5 CRC64;
                                                                                                                                                                                                      Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Akashi K.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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Parani M., Parida A.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AB182918; BAD26571.1; -...
GO; GO:0046872; F:metal ion binding; IEA.
InterPro; IPR000347; Metallthion_15p.
Pfam, PF01439; Metallthion_15p.
ProDom; PD011611; Metallthion 15p; 1...
SEQUENCE 77 AA; 7805 MW; GE75AB740535B64 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Type-2 metallothionein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                      DB 2;
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                                                                                                                                                                                                      2.2%; Score 8; DB 2
100.0%; Pred. No. 9.6
:ive 0; Mismatches
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100.0%; Pred. No. 9.6
:ive 0; Mismatches
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                                                                                                                                                                                    Query Match
Best Local Similarity 100...
Rest Local 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                 302 CGGNCGCG 309
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
NCBI_TaxID=84609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                  Q61674
Q61674;
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SORRESERVEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: Metallothioneins have a high content of cysteine residues that bind various heavy metals.
-!- SIMILARITY: Belongs to the metallothionein superfamily. Family 15.
                                                                                                                                                                                                                                                                                                                                                      Trifolium repens (Creeping white clover).
Eukaryota, Viridiplantee, Streptophytes, Embryophytes, Tracheophytes, Spermatophytes, Mayonoliophytes, eudicotyledons; core eudicots; rosids; eurosids I: Fabales; Fabaceae; Papilionoideae; Trifolium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=cv. Huia; TISSUE=Stolon node;
Ellison N.W., White D.W.R.;
IIsolation of two Calones encoding metallothionein-like proteins
from Trifolium repens L.";
(er) Plant Gene Register PGR96-068.
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name-AzMT2;
Azolla filiculoides (Water fern).
Eukaryoua; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Moniliformopses; Filicophyta; Filicopsida; Hydropteridales;
Azollaceae; Azolla.
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                                                     ö
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0: Indels
               Length 77;
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Probom; PD001611; MetallthTon 15p; 1.
Metal-binding; Metal-thiolate cluster; Multigene family.
SEQUENCE 77 AA; 7503 MW; 5F4C163BA644BBD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 77;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
02-CCT-2004 (Rel. 45, Last annotation update)
Metallothionein-like protein A (MT-A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 AA.
                                                                                                                                                                                                                        77 AA
             Query Match
2.2%; Score 8; DB 1
Best Local Similarity 100,0%; Pred. No. 9.6
Best Ches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.2%; Score 8; DB 1
100.0%; Pred. No. 9.6
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000347; Metallthion_15p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metallothionein-like protein 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z26492; CAA81264.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                        STANDARD;
                                                                                       302 CGGNCGCG 309
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                                                                                                                          4 CGGNCGCG 11
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Best Local Similarity
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                                                                                                                                                                                                                    MTA_TRIRP
P43398;
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FROM N.A.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Eichhornia crassipes metallothionein-like protein, clone C (Eichhornia crassipes metallothionein-like protein, clone A) (Eichhornia crassipes metallothionein-like protein, clone A) (Eichhornia crassipes metallothionein-like protein, clone B) (Metallothionein).
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                             Gaps
                                                                                                                                                                                                                                            Name=WT1;
Elchhornia crassipes (Water hyacinth).
Elchhornia crassipes (Water hyacinth).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Commelinales;
Pontederiaceae; Elchhornia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=MTI;
Bichhornia crassipes (Water hyacinth).
Bichkornia crassipes (Water hyacinth).
Spermatophyta; Magnoliophyta; Liliopsida; Commelinales;
Pontederiaceae; Eichhornia.
NCBI_TaxID=44947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Parani M., Parida A.;
Submitted (DEC-2000) to the BMBL/GenBank/DDBJ databases.
EMBL; AF334141; AAK11269.1; -.
EMBL; AF329968; AAG61122.1; -.
GD; GO:0046872; F:metal ion binding; IEA.
InterPro; IPR000347; Metallthion 15p.
Pfam; PF01439; Metallothio 2; 1.
Probom; PD001611; Metallthion 15p; 1.
Probom; PD001611; Metallthion 15p; 1.
                                                                                                            0; Indels
                                                                                          Length 77;
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Last annotation update)
                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                  2.2%; Score 8; DB 2;
100.0%; Pred. No. 9.6;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 AA.
                                                                                          2.2%; Score 8; DB 2
100.0%; Pred. No. 9.6
:ive 0; Mismatches
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                                                                                                                                                                                                           Created)
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                   Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
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                                                                                                                              302 CGGNCGCG 309
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Best Local Similarity
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Metallothionein.
                                                                                           Query Match
                                                                                                                                                                                          Q9SMG3
Q9SMG3;
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Q9SMG3
ID Q9SMG:
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Matches
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Q9ZNT5
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 41, Last annotation update)
Metallothionein-like protesin type 2.
Nicotiana glutinosa (Tobacco).
Eukaryorat, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; asterids;
lamiids; Solanates; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Choi D., Kim H.M., Yun H.K., Yi S.Y., Bok S.H.;
Submitted (JAN-1996) to the EMBL/GenBank/DBBJ databases.
-!- FUNCTION: Metallothioneins have a high content of cysteine
residues that bind various heavy metals.
-!- SIMILARITY: Belongs to the metallothionein superfamily. Family 15.
                                                                                                                                                                                                                            TISSUE=Root;
Kong K.F., Tsang J.S.H.;
Kong K.F., Tsang J.S.H.;
"Nucleotide Sequences of Genomic Clones (Accession Nos. AJ247090,
AJ247195 and AJ247196) Encoding a Type 2 Metallothionein-like Protein
from Water Hyacinth (Eichhornia crassipes). (PGR99-143).";
                               Kong K.F., Tsang J.S.;
"Nucleotide sequence of cDNAs encoding metallothionein-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5069A650ED3CC8F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8B78CDCFABD4A809 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.2%; Score 8; DB 2;
100.0%; Pred. No. 9.6;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     Plant Physiol. 121:313-313(1999).

EMBL; AJ010162; CAA09025.1; --
EMBL; AJ010160; CAA09023.1; --
EMBL; AJ040160; CAA09024.1; --
EMBL; AJ247090; CAB53390.1; --
GMBL; AJ247090; CAB53390.1; --
GMBL; AJ247090; P:metal ion binding; IEA.

InterPro; IPR000347; Metallthion_15p.
Prodom; PP00411; Metallthion_15p.

SEQUENCE 77 AA; 7885 MW; 5069A650ED3CC8
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Pfam; PF0439; Metallothio 2; 1.
ProDon PD001611; Metallthion_15p; 1.
ProDon pd0199; Metal-thion_15p; 1.
                                                                                                                             Plant Physiol. 118:1101-1101(1998)
MEDLINE=99105148; PubMed=9890811;
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Matches 8; Conservative
                                                                                              from water hyacinth.";
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                                                                                                                                                                                                SEQUENCE FROM N.A.
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78 AA

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Codonopsis lanceolata.

Bukazyophyta; Varidiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
campanulids; Asterales; Campanulaceae; Codonopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Populus baltamifera subsp. trichocarpa x Populus deltoides.
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; rosids;
eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Kohler A., Blaudez D., Chalot M., Martin F.;

Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; AYS94298; AAT02252.1; -.

GO; GO:0046872; F:metal ion binding; IEA.

InterPro; IPR000347; Metallthion_15p.

Ffam; PF01439; Matallthion_15p.

PRODOM; PD001611; Metallthion_15p.

PRODOM; P001611; Metallthion_15p.

SEQUENCE 78 AA; 7901 MW; B43DECB278B82ADD CRC64;
                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last annotation update)
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100.0%; Pred. No. 9.8;
ve 0; Mismatches
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Pred. No.
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(TrEMBLrel. 27, Last seq
(TrEMBLrel. 27, Last ann
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100.0%; Pre
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100.0%; Pre
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27,
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nes 8; Conservative
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                                                                                                                                                                         PRELIMINARY;
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4 CGGNCGCG 11
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Matches 8; Conserv
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TISSUE=Branch;
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Best Local S
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QEPML3;
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Q6L8H8
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                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Metallothionein-like protein type 2.
Narcissus pseudonarcissus (Daffodia).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
                                Gaps
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Bopermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Amaranthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUB-Senecing tepals of 4-day old flowers,
Hunter D.A., Steele B.C., Reid M.S.;
Hunter D.A., Steele B.C., Reid M.S.;
Hunter D.A., Steele B.C., Reid M.S.;
Aldentification of genes associated with perianth senescence in
daffodil (Narcissus pseudonarcissus L. 'Dutch Master').";
Plant Sci. 163:13-21(2002).
PMBL; AF42001; AAL16908.1;
GO, GO:0046672; Fixeral ion binding; IEA.
InterPro; IPR000347; Metallthion.15p.
Pfam; PP01439; Metallthio.2; 1.
ProDom; PD001611; Metallthio.15p; 1.
SEQUENCE 78 AA; 7708 MW; 149B73425AEDB321 CRC64;
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RESULT 1 ADK68116

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The nucleic acid molecules, polypeptides and antibodies are useful for treating, preventing or diagnosing diseases such metabolic disorders, diabetes, obselty, infectious diseases (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer, cardiovascular diseases (hypertension, atherosclerosis), morexia, cancer, cardiovascular diseases (hypertension, atherosclerosis), immune disorders, Alzheimer's disease, Parkinson's disease, epilepsy, immune disorders, Alzheimer's costeoarthritis), hematopoietic disorders, inflammatory skin disorders, asthma, and various dyslipidemias. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that confibration, hematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridization probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. This sequence corresponds to one of the NOVX proteins of the invention.
to, or having one or more conservative amino acid substitutions in, the proteins. The polypeptides, nucleic acid molecules and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOVX; human; cardiomyopathy; atherosclerosis; hypertension; pulmonary stenosis; obesity; prostate cancer; diabetes; haemophilia; skin disorder; graft versus host disease; AIDS; asthma: lupus; Crohn's disease; inflammatory bowel disease; ulcerative colitis; multiple sclerosis; infectious disease; anorexia; Alzheimer's disease; Parkinson's disease; NOV4c.
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Stone DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel NOVX protein and their encoding DNA's, mature forms of the proteins or sequences that are at least 95% identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Casman SJ;
רבי RR, Gerlach VL;
  Adb46934 Novel hum
Adb86541 Human PRO
                                                                                                                                                                                                                                                                                                                                                                     antidiabetic; anorectic; cardiant; hypotensive; antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic; neuroprotective; antiparkinsonian; anticonvulsant; osteopathic; antiartritic; antiniflammatory; dermatological; antiasthmatic; antiliflammatory; dermatological; antiasthmatic; antiliflammatory; dermatological; antiasthmatic; infectious disease; anorex; cardiovascular disease; hypertension; atherosexia; cancer; cardiovascular disease; hypertension; atheroseric disease; perkinson's disease; epilepsy; immune disorder; osteoarthritis; hematopoietic disorders; inflammatory skin disorder; asthma; dyslipidemia; neurogenesis; cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alsobrook JP, Bento P, Boldog FL, Burgess CE, Casman SJ; Crabtree-Bokor JR, Edinger SR, Ellerman K, Fernandes ER, Gerosse WM, Guthther E, Gusev VY, Heyes MP, Lepley DM, Li L; Macdougall JR, Malyankar UM, Millet I, Patturajan M, Peyman Rastelli L, Rieger DK, Shenoy SG, Shimkets RD, Smithson G.
                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 42; 323pp; English.
ADB46934
ADB86541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome mapping; pharmacogenomic
                                                                                                                                                                                                 ADK68116 standard; protein; 123 AA
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2002US-0384297P.
2002US-0384329P.
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2002US-0370279P.
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2002US-0374379P.
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2003US-00403142
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                                                                                                                                                                                                                                                                                      (first entry)
  364
                                                                                                                                                                                                                                                                                                                                  Novel NOVX protein #21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  asthma, or infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-812730/76.
100.0
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30-MAY-2002;
30-MAY-2002;
17-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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22-APR-2002;
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Gaps

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(first entry)

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VEGF-E; platelet derived growth factor; PDGF; FCTRX; hyperplassa; cancer; neoplassa; anaemia; leukopenia; baldness; cardiovascular disorder; fibrotic disorder; diabetic ulcer; obesity; hyperproliferation; human; dysproliferation; neurodegenerative disorder; osteoarthritis; epilepsy; inflammatory disorder; Graft versus host disease; coagulation; haemophilia; neural disorder; Parkinson's disease; Alzheimer's disease; multiple sclerosis; Huntington's disease; amyotrophic lateral sclerosis;
                                                                                                                                                                 morphogenetic protein-1; BMP-1; vascular endothelial growth factor
   71 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIOLDHHERCDCICSSRPPR 123
                                                                                                                                       Human FCTR2 protein present in clone 30664188.0.331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shimkets RA, Lichenstein H, Herrmann JL,
                                                                                                                                                                                                                                                                 peripheral neuropathy; acute brain injury.
                                                              AAU00699 standard; protein; 132
                                                                                                                                                                                                                                                                                                                                                                                       07-OCT-1999; 99US-0158083P.
13-OCT-1999; 99US-0158231P.
04-JAN-2000; 2000US-0174485P.
03-MAR-2000; 2000US-0186707P.
10-MAR-2000; 2000US-0186707P.
11-SEP-2000; 2000US-023879P.
12-SEP-2000; 2000US-00662783.
                                                                                                                                                                                                                                                                                                                                                                 06-OCT-2000; 2000WO-US027671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CURA-) CURAGEN CORP.
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                                                                                                              07-SEP-2001
                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                       AAU00699;
                                      RESULT 3
                                                   AAU00699
  d
                                                                           polynucleotides encoding them. The therapeutic is useful in the manufacture of a medicament for treating a syndrome associated with a human disease selected from pathology associated with the polypeptide. Diseases include cardiomyopathy, atherosclerosis, hypertension, pulmonary stenosis, obesity, prostate cancer, diabetes, haemophilia, skin disease, inflammancry bowel disease, locarative colitis, multiple sclerosis, inflammancry bowel disease, ulcerative colitis, multiple sclerosis, infectious disease, anorexie, Alzheimer's disease, or Parkinson's disease. They are also useful in detection assays, chromosome mapping, or tissue typing. This sequence represents the human NOV4c
                                                                                                                                                                                                                                                                                                                                                                                                   J, Bento P, Boldog F, Burgess C, Casman S, Bokor JC; R, Ellerman K, Fernandes E, Gerlach V, Grosse W, Gunther E; Heyes M, Lepley D, Li L, Macdougall JR, Malyankar UM; Parturajan M, Peyman JA, Rastelli L, Rieger D, Shenoy S; R, Smithson G, Stone D, Vernet C, Voss E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preventing, e.g. cardiomyopathy, atherosclerosis, hypertension, obesity, prostate cancer, diabetes, hemophilia, AIDS, inflammatory bowel disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polypeptides and nucleic acids, useful for treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel human NOVX polypeptides and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 42; 206pp; English.
 15-AUG-2002; 2002US-0403748P.
                                                                                                                                                                                                                        MACDOUGALL J R
MALYANKAR U M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infectious disease.
                                                                                                                                                                                                                                                              PATTURAJAN M.
                                                                                   BOKOR J C.
EDINGER S R.
                                                                                                                                                                                                                                                                          PEYMAN J A.
RASTELLI L.
                                                                                                                        FERNANDES E.
GERLACH V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-603580/58.
                                                                                                              ELLERMAN K.
                                                                                                                                                                                                                                                                                                                          SHIMKETS R.
SMITHSON G.
                                                BOLDOG F.
BURGESS C.
CASMAN S.
                                                                                                                                                GROSSE W.
GUNTHER E.
GUSEV V.
HEYES M.
                                                                                                                                                                                                                                                                                                                                                STONE D.
VERNET C.
                                                                                                                                                                                                  LEPLEY D.
                                                                                                                                                                                                                                                                                                     RIEGER D.
SHENOY S.
                                                                                                                                                                                                                                                    MILLET I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADR49104
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                                                                                                                                       GERLACH
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Shimkets R,
                                                                                                                                                                                                                                                                                                                                                                                                                 Edinger SR,
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(VERN/)
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(EDIN/)
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DOSSING

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The sequence represents a protein related to bone morphogenetic protein-1 (BMP-1), vascular endothelial growth factor (VEGF-E) and platelet derived growth factor (PDGF). Polypeptides and polynucleotides related to BMP-1, VEGF-E and PDGF are referred to as FCTRX peptides and nucleic acids.

VEGF-E and PDGF are referred to as FCTRX peptides and nucleic acids.

FCTRX proteins are useful for treating or preventing a disorder.

FCTRX proteins are useful for treating or preventing a disorder.

FCTRX proteins are useful for treating or preventing a disorder is characterised by insufficient or ineffective growth of a cell physiological interactions of the proteins in a mammal, where the disorder is characterised by insufficient or ineffective growth of a cell as characterised and intreatment of cancer, anaemia, associated nucleic acids are useful for both promoting and inhibiting growth of cells and tissues and in treatment of cancer, anaemia, and tissues and in treatment of cancer, anaemia, calabetic ulcers, obesity, infectious diseases, hyperpoliferative disorders, neurodegenerative disorders, neurodegenerative disorders, osteoarthritis, inflammatory disorders, neurodegenerative disorders, costeoarthritis, such as haemophilia, and neural disorders including Parkinson's disease, and ephlepsy and ephlepsy and ephlepsy
Novel growth factor polypeptides termed as FCTRX polypeptides, useful for treating cancer, cardiovascular and fibrotic diseases, diabetic ulcers, wound healing and neuronal disorders.
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Gaps

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1 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT 11 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT

100.0%; Score 631; DB 8; Length 123; larity 100.0%; Pred. No. 3.2e-62; Conservative 0; Mismatches 0; Indels (

Local Similarity es 113; Conserv

Best Loca Matches

Query Match

CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 113

61

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Boldog FL, Minskoff S;

AA;

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Sequence 132
                        Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the protein sequence of human FCTR2, as predicted from a cDNA clone isolated from pituitary gland tissue. The sequence is identical to the creminal region of FCTR1 (see ABB79643), also referred to as platelet derived growth factor D. suggesting the 2 proteins to be products of splice variants of a common gene. FCTR2 shows similarity to human growth factor FIGF (c-fos-induced growth factor) and to rat vascular endothelial growth factor D. The invention provides FGFCX and FCTRX growth factors, polypeptides and deletion variants, and methods of using these to treat, delay the onset of, or ameliorate, an inflammatory pathology, especially inflammatory bowel disease, a disease that occurs in the colon or small intestine, or Crohn's disease (all claimed). The FGFCX and FCTRX polypeptides and polynucleotides are also useful for treating growth and proliferative diseases such as cancer, angiogenesis, collagen formation, fibrotic and cardiovascular diseases or diabetic claims methods, chromosome mapping, tiseue typing, predictive medicine, diagnostic assays, and pharmacogenomics
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3, Larochelle WJ, Lichenstein HS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating, delaying the onset of, or ameliorating an inflammatory pathology (e.g. inflammatory bowel disease or Crohn's disease) by administering to the subject fibroblast growth factors or a combination of growth factors.
                                                                                                                                                                                                                                                                                                                                   FCTR2; platelet derived growth factor D; PDGFD; human; Crohn's disease; inflammatory bowel disease; gene therapy; antiinflammatory; vulnerary; cytostatic; cardiovascular.
                                                                                       VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
                                                                                                               20 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVORCGGNCGCGTVNWRSCT
                                                               Gaps
                                                                                                                                        CNSGKTVKKYHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 113
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                                     Length 132;
                                                              Indels
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                                    Score 631; DB 4;
Pred. No. 3.5e-62;
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                                                            Mismatches
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Shimkets JB,
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                                                                                                                                                                                                                                 ABB79644 standard; protein; 132
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                                   100.0%;
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                                                                                                                                                                                                                                                                                   (first entry)
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Fernandes ER, Rittman B,
                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CURA-) CURAGEN CORP.
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N-PSDB; ABN84525.
                                               Best Local Similarity
Matches 113; Conserv
            Sequence 132 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                   WO200258716-A2
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                    21-OCT-2002
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                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a new method of detecting the presence of 30664188 antigen in a sample. The invention is useful for detecting the presence of 30664188 in a biological sample (e.g. blood or its component originating from a mammal, preferably human), and for contributing to diagnosis of cancer in a subject. The present amino acid sequence represents a human FCTR protein, as described in the methods of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting presence or amount of 30664188 antigen in a sample, by contacting the biological sample with agent that binds the antigen, and detecting the presence or amount of agent bound to the antigen.
                                                                                                                            20 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFPPRCLLVQRCGGNCGCGTVNWRSCT
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                                                                                               1 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
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  Length 132;
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                                                 Indels
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100.0%; Score 631; DB 5;
100.0%; Pred. No. 3.5e-62;
ive 0; Mismatches 0;
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100.0%; Pred. No. 3.5e-62;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30664188 antigen; blood; cancer; human; FCTR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 15-16; 177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Larochelle W;
                                                                                                                                                                                                                                                                                                                                                                            ABG78503 standard; protein; 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-NOV-2001; 2001WO-US048901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-NOV-2000; 2000US-00715332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lichenstein H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 113; Conservative
                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Andrews D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human FCTR 2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-619187/66.
N-PSDB; ABS63516.
                    Local Similarity
nes 113, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200259618-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jeffers M,
                                                                                                                                                                                                                                                                                                                                                                                                                           ABG78503;
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diabetes, obesity, infectious diseases (viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                       Sequence 132 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lichenstei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADM57645;
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(BURG/)
(FERN/)
(JEFF/)
(LARO/)
(LICH/)
(PETE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (RITT/)
(SHIM/)
(SHIM/)
(YANG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADM57645
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88000000000000080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel NOVX protein and their encoding DNA's, mature forms of the proteins or sequences that are at least 95% identical to, or having one or more conservative amino acid substitutions in, the proteins. The polypeptides, nucleic acid molecules and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The nucleic acid molecules, polypeptides and antibodies are useful for treating, preventing or disgnosing diseases such metabolic disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alsobrook JP, Bento P, Boldog FL, Burgess CE, Casman SJ; Crabtree-Bokor JR, Edinger SR, Ellerman K, Fernandes ER, Gerlach VL; Grosse WM, Gunther E, Gusev VY, Heyes MP, Lepley DM, Li L; Madougall JR, Malyankar UM, Millet I, Patturajan M, Peyman JA; Rastelli L, Rieger DK, Shenoy SG, Shimkets RD, Smithson G, Stone DJ; Vernet CAM, Voss EZ;
                                                                                                                                                                                                                                             antidiabetic; anorectic; cardiant; hypotensive; antiarteriosclerotic; norectic; virucide; antibacterial; fungicide; protozoacide, noctropic; neuroprotective; antibacterial; fungicide; protozoacide, noctropic; antiarthritic; antiinflammatory; dermatological; antiasthmatic; antiarthritic; antiinflammatory; dermatological; antiasthmatic; antiarthritic; ache therapy; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer, cardiovascular disease; hypertension; atheroselerosis; neurodegenerative disorder; hypertension; atheroselerosis; neurodegenerative disorder; osteoarthritis; hematopoietic disorders; inflammatory skin disorder; asthma; dyslipidemia; neurogenesis; cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 38; 323pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome mapping; pharmacogenomic.
                                                               ADK68112 standard; protein; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-APR-2002; 200203-0370279P.
05-APR-2002; 200205-0370359P.
06-APR-2002; 200205-0370359P.
12-APR-2002; 200205-0370369P.
12-APR-2002; 200205-0374379P.
15-MAY-2002; 200205-0384237P.
30-MAY-2002; 200205-038429P.
17-JUN-2002; 2002U5-0389729P.
17-JUN-2002; 2002U5-0389729P.
13-AUG-2002; 2002U5-0389729P.
15-AUG-2002; 2002U5-0389729P.
15-AUG-2002; 2002U5-0403491P.
15-AUG-2002; 2002US-040349P.
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                                                                                                                                                          (first entry)
                                                                                                                                                                                                      Novel NOVX protein #19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       asthma, or infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-812730/76.
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05-APR-2002;
                                                                                                                                                          06-MAY-2004
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                                                                                                              ADK68112;
                   RESULT 6
ADK68112
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helminthic, and procozoal), anorexia, cancer, cardiovascular diseases (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's disease, extrinson's disease, epilepsy, immune disorders as tarkinson's disease, epilepsy, immune disorders skin disorders, asthma, and various dyslipidemias. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, hematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridization probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. This sequence corresponds to one of the NOVX proteins of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Larochelle WJ;
, Shimkets JB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 CNSGKTVKKYHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 631; DB 7; Length 132; 100.0%; Pred. No. 3.5e-62; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             iss CE, Fernandes ER, Jeffers ME, L
Peterson J, Prayaga SK, Rittman B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADM57645 standard; protein; 132 AA
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06-JUN-2002; 2002US-0386545P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 113; Conservative
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BURGESS C E.
FERNANDES E R.
JERRENS M E.
LAROCHELLE W J.
LICHENSTEIN H S.
PETERSON J.
PRAYAGA S K.
RITIMAN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burgess CE,
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SHIMKETS R A.
YANG M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human FCTR2 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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MACDOUGALL J R. MALYANKAR U M. MILLET I. PATTURAJAN M.

LEPLEY D.

PEYMAN J A. RASTELLI L.

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BOKOR J C.
EDINGER S R.
ELLERMAN K.
                                                                      FERNANDES E
GERLACH V.
GROSSE W.
BENTO P.
BOLDOG F.
BURGESS C.
CASMAN S.
                                                                                                   GUNTHER E.
GUSEV V.
HEYES M.
                                                                                                                                                                                                           (RIEG/)
(SHEN/)
                                                                                                                                                                                                                                                    (SMIT/)
(STON/)
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           (BOLD/)
(BURG/)
(CASM/)
                                                 (ELLE/)
                                                                       FERN/)
                                                                                  (GERL/)
(GROS/)
                                                                                                                                                        (MACD/)
                                                                                                                                                                   (MALY/)
                                                                                                                                                                                                 (PEYM/)
                                                                                                                                                                                                                                                                       (VERN/)
                                                                                                                GUSE/
                                          BOKO/
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                                                                                                       GUNT/
                                                                                                                                     TEPL/
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                    Promoting the growth of a population of cells, useful for treating inflammatory conditions, comprises contacting the at least one cell with a composition comprising FGFCX and/or FCTRX polypeptides.
                                                                                                                                                                                                                                                                      79
                                                                              The present invention is based upon methods of treating inflammatory conditions in the intestinal tract of mammala using fibroblast growth factor (FGP)-CX and/Or FCTRX(undefined) polypeptides and their encoding polynucleotides. The invention is useful for treating inflammatory pathology such as inflammatory bowel disease, inflammatory condition occurring in the colon or small intestine and Crohn's disease. The invention is also useful in gene therapy. The present sequence is human FCTRX protein. The sequence is also referred as human platelet-derived growth factor D (PDGFD) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                NOVX; human; cardiomyopathy; atherosclerosis; hypertension; pulmonary stenosis; obesity; prostate cancer; diabetes; haemophilia; skin disorder; graft versus host disease; AIDS; asthma; lupus; Crohn's disease; inflammatory bowel disease; ulcerative colitis; multiple sclerosis; infectious disease; anorexia; Alzheimer's disease;
                                                                                                                                                                                                                                                    1 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
                                                                                                                                                                                                                                                                      VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
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0
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                                                                                                                                                                                                           Length 132;
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                                                                                                                                                                                                          100.0%; Score 631; DB 8;
100.0%; Pred. No. 3.5e-62;
live 0; Mismatches 0;
                                                           Claim 4; SEQ ID NO 6; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                   ADR49101 standard; protein; 132 AA
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2002US-0370969P.
2002US-0372019P.
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15-MAY-2002; 2002US-0380973P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parkinson's disease; NOV4a
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              Human NOV4a protein.
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                                                                                                                                                                                        Sequence 132 AA;
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08-APR-2002;
12-APR-2002;
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                                                                                                                                                                                                                                                                                           Gunther E;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polypeptides and nucleic acids, useful for treating or preventing, e.g. cardiomyopathy, atherosclerosis, hypertension, obesity, prostate cancer, diabetes, hemophilia, AIDS, inflammatory bowel disease, or infectious disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 VDLDRINDDAKRYSCTPRNYSVNIRBELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
                                                                                                                                                                                                                                  Alsobrook J, Bento P, Boldog F, Burgess C, Cabusto, Grosse W, Gunth Edinger SR, Ellerman K, Fernandes E, Gerlach V, Grosse W, Gunth Gusev V, Heyes M, Lepley D, Li L, Macdougall JR, Malyankar UM, Millet I, Patturajan M, Peyman JA, Rastelli L, Rieger D, Sheno Willet I, Patturajan M, Peyman JA, Rastelli L, Rieger D, Sheno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        2004-603580/58.
RIEGER D.
SHENOY S.
SHIMKETS R.
SMITHSON G.
STONE D.
VERNET C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADR49100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 132 AA;
                                                                                                                                                                                                 VOSS E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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Sequences ABB10981-ABB12310 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a mucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may consider activities, including cytokine, cell proliferation or cell differentiation activities; including cytokine, cell proliferation or cell differentiation activities; seem cell growth factor activity; chancedulatory activity; activin- or inhibin-related activities; chancedulatory activity; activin- or inhibin-related activities; chancedulatory activity; activin- or inhibin-related activities; chancedulatory activities; preceptor or ligand activities; or metastasis.

Compound an encourage of activities; preceptor or ligand activities or metastasis.

Conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions and abnormal conditions, activities are therapy. Such conditions activities are therapy. Such conditions and abnormal conditions are useful for general egg., activity activities (e.g., activity are regeneration and anormal areticities and all proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., coronary heart disease, arterial ischaemia, bone disorders (e.g., coronary heart disease).
                                                                                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; growth factor; hematopodesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; proliferation; call disorder; lymphoid cell disorder; asthma; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis
                                                                                                                                                                                                                                                                                                                                                                               bone disorder; osteoporosis; vascular growth disorder;
tissue regeneration; wound healing; infection; immune disorder;
cell culture; drug screening; gene therapy; antiinflammatory;
antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
antifungal; vulnerary; antiulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; Page 229; 1963pp; English.
                                                                                                                                                                   Human novel grotein, SEQ ID NO:2067.
                      ABB11697 standard; peptide; 152 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mars week
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT;
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27-APR-2000; 2000US-00560875.
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                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABA08941.
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                                                                                                                    11-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and cancer
                                                                     ABB11697;
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ABB11697
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         healing (e.g., of burns, incidence and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug soreening techniques. The present sequence represents a novel human polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bone morphogenetic protein-1; BMP-1; vascular endothelial growth factor; VBGP-E; platelet derived growth factor; PDGF; FCTRX; hyperplasia; cancer; neoplasia; anaemia; leukopenia; paldness; cardiovascular disorder; fibrotic disorder; dabetic ulcer; obesity; hyperproliferation; human; dysproliferation; neurodegenerative disorder; osteoarthritis; epilepsy; harmory disorder; Graft versus host disease; coagulation; haemophilia; neural disorder; Parkinson's disease; Alzheimer's disease; multiple sclerosis; Huntington's disease; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                            40 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVORCGGNCGCGTVNWRSCT
                                                                                                                                                                                                                                                                                                                                          1 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
                                                                                                                                                                                                                                                                                                         Gapa
 repair (or nucleic acids encoding them) may be used to promote wound
                                                                                                                                                                                                                                                                                                                                                                                                                                100 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 152
                                                                                                                                                                                                                                                                                                                                                                                                               61 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 113
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                                                                                                                                                                                                                                                                     Length 152;
                                                                                                                                                                                                                                                                                                       Indels
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0
                                                                                                                                                                                                                                                                   100.0%; Score 631; DB 4; 100.0%; Pred. No. 4.1e-62;
                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Mature FCTR5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU00702 standard; protein; 154 AA
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13-0CT-1999; 99US-0159231P.
04-JAN-2000; 2000US-017485P.
03-MAR-2000; 2000US-0186707P.
10-MAR-2000; 2000US-0188259P.
08-AUG-2000; 2000US-023379P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-SEP-2000; 2000US-00662783.
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                                                                                                                                                                                                                                                                                                     Matches 113; Conservative
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                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                  Seguence 152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200125437-A2
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                                                                                                                                                                                                                                                                     Query Match
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06-NOV-2001; 2001WO-US043846.
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                                                                                                                                               The sequence represents a protein related to bone morphogenetic protein-1 (BMP-1), vascular endothelial growth factor (WEG-E) and platelet derived growth factor (PDGF). Polypeptides and polymcleotides related to BMP-1, vescular endothelial growth factor (BDGF).

C WEGF-E and PDGF are referred to as FCTRX petides and nucleic acids.

C WEGF-E and PDGF are useful for treating or preventing a disorder.

C FCTRX proteins are useful for treating or preventing a disorder aberrant expression, aberrant processing, or aberrant comparing of the proteins in a mammal, where the disorder is characterised by insufficient or ineffective growth of a cell or a sesociated nucleic acids are useful for both promoting and their associated nucleic acids are useful for both promoting and inhibiting clerophia, baldness, for treating cardiovascular and fibrotic disorders, diabetic ulcers, obesity, infectious diseases, hyperproliferative and disorders, neurodegenerative disorders, neurodegenerative disorders, of after versus host disease, capulation disorders such as haemophila, and neural disorders including Parkinson's disease, and or any particular and previous disease, multiple sclerosis, Huntington's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                          Novel growth factor polypeptides termed as FCTRX polypeptides, useful for treating cancer, cardiovascular and fibrotic diseases, diabetic ulcers, wound healing and neuronal disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCTR5; platelet derived growth factor D; PDGFD; human; Crohn's disease; inflammatory bowel disease; gene therapy; antlinflammatory; vulnerary; cytostatic; cardiovascular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 154
 Minskoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 631; DB 4; Length 154; 100.0%; Pred. No. 4.1e-62; ive 0; Mismatches 0; Indels (
 Boldog FL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human FCTR5 (platelet derived growth factor D).
Lichenstein H, Herrmann JL,
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/label= Signal_peptide
24. 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24. 154
/label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB79647 standard; protein; 154 AA
                                                                                                                          Claim 1; Page 19; 171pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 113; Conservative
                                      2001-316172/33
                                                  N-PSDB; AAS04496
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200258716-A2
 Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                       epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-OCT-2002
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              Jeffers M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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The present sequence is the protein sequence of FCTRS, also referred to as platelet derived growth factor D (PDGFD) or human PDGFD. FCTRS is a splatelet derived growth factor D (PDGFD) or human PDGFD. FCTRS is a classification signal peptide, PDGF domain and N-Q1ycosylation site. Human FCTRS is most closely related to human PDGF C, B and A. The invention provides FGFCX and FCTRX growth factors, polypeptides and variants, and polymclectides conciding them, an inflammatory pathology, especially inflammatory bowel disease, a disease that occurs in the colon or small intestine, or crohn's disease (all claimed). The FGFCX and FCTRX polypeptides and polymclectides are also useful for treating growth and proliferative diseases such as cancer, angiogenesis, collagen formation, fibrotic and cardiovascular diseases or diabetic ulcers, and in wound healing. They can be used in screening and detection methods, chromosome mapping, tissue typing, predictive medicine, diagnostic assays, prognostic assays,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101
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                                                                                                                                                               Lichenstein HS;
                                                                                                                                                                                                                                                                                                                           Treating, delaying the onset of, or ameliorating an inflammatory pathology (e.g. inflammatory bowel disease or Crohn's disease) by administering to the subject fibroblast growth factors or a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fibroblast growth factor-CX; FGF-CX; FCTRX; inflammatory bowel disease;
                                                                                                                                   Burgess CE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 154;
                                                                                                                                oldog FL, Yang M,
Larochelle WJ, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24. :154 - /note= "Human mature FCTR5 protein"
                                                                                                                                   Boldog FL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 631; DB 5; 100.0%; Pred. No. 4.1e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammation, Crohn's disease, gene therapy, platelet-derived growth factor; PDGFD; human.
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                                                                                                                                Prayaga S, Bo
Shimkets JB,
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Page 26; 196pp; English.
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06-NOV-2000; 2000US-0246206P
                                                                                                Shimkets RA, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 113, Conservative
                                                                                                                                                                  Fernandes ER, Rittman
                                                                 (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and pharmacogenomics
                                                                                                                                                                                                                                 2002-599742/64.
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                                                                                                                                                                                                                                                                                                                                                                                                                               growth factors.
                                                                                                                                                                                                                                                                N-PSDB; ABN84528
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The invention relates to an isolated protein comprising a first polypeptide disulphide-bonded to a second polypeptide. The first and second polypeptides are from 113-138 amino acid residues and comprises 256-370 amino acid residues of human growth factor homologue ZVBGF4. The protein stimulates proliferation, differentiation, or migration of protein stimulates proliferation, differentiation, or migration of semanhorins. ZVBGF4 may be used to design ant/agonists of neuropilin-companient development, cartilage and limb development. T- and B-cell cuncer, autoimmune diseases, inflammation, retinopathies, haemangiomas, cardiovascular development, cartilage and limb development. T- and B-cell cuncer, autoimmune diseases, inflammation, retinopathies, haemangiomas, system diseases and peripheral nervous system diseases and peripheral nervous system diseases including stroke. The isolated protein is also used for a pharmaceutical composition as cherapeutic agents, diagnostic agents, and research tools and reagents. It can be used in the study and regulation of cell and tissues to control organ component, as components of cell culture media. The proteins can form development by modulating cell proliferation, migration, differentiation, or metabolism. The gene for human ZVEGF4 is located on chromosome 11922.3 crossing but not further defined in the specification).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated growth factor analogue ZVEF4 proteins for pharmaceutical composition as, e.g. therapeutic agents, diagnostic agents, and research tools and reagents, includes polypeptides from amino acid residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
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                  autoimmune disease; inflammation; retinopathy; haemangioma; ischaemic event; neuropathy; acute nerve damage; stroke; central nervous system disease; peripheral nervous system disease.
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100.0%; Pred. No. 8.8e-62;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                             03-MAY-1999; 99US-0132250P.
10-NOV-1999; 99US-0164463P.
04-FEB-2000; 2000US-0180169P.
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Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              Gilbert T, Hart CE,
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                                                                                                          Unidentified
                                                                                                                                                   US6495668-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Promoting the growth of a population of cells, useful for treating inflammatory conditions, comprises contacting the at least one cell with a composition comprising FGFCX and/or FCTRX polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conditions in the intestinal tract of mammala using fibroblast growth factor (FGF)-Cx and/or FCTRX (undefined) polypeptides and their encoding polynucleotides. The invention is useful for treating inflammatory pathology such as inflammatory bowel disease, inflammatory condition occurring in the colon or small intestine and Crohn's disease. The invention is also useful in gene therapy. The present sequence is human FCTRX protein. The sequence is also referred as human platelet-derived growth factor D (PDGFD) cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention is based upon methods of treating inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Larochelle WJ;
Shimkets JB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Growth factor homologue, ZVEGF4, proliferation, differentiation, migration, mesenchymal cell; cell surface semaphorin, neuropilin, neurite growth, cardiovascular development, limb development;
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Prayaga SK, Rittman B,
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Pred. No. 4.1e-62;
0; Mismatches 0;
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HS, Peterson J,
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100.0%;
                                                                                                                            16-NOV-2001; 2001US-00011364
                                                                                   16-DEC-2002; 2002US-00321962
                                                                                                                                                2002US-0386545P
                                                                                                                                                                                       BOLDOG F L.
BURGESS C E.
FERNANDES E R. I
                                                                                                                                                                                                                                                                           LAROCHELLE W J.
LICHENSTEIN H S.
PETERSON J.
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Best Local Similarity 100.
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                             PRAYAGA S K.
RITTMAN B.
SHIMKETS J B.
SHIMKETS R A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2004-081737/08.
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US2004006015-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                     YANG M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lichenstein HS,
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                                                                                                                                                06-JUN-2002;
                                        08-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                   (RITT/)
(SHIM/)
(SHIM/)
(YANG/)
                                                                                                                                                                                                                                                                             (LARO/)
(LICH/)
(PETE/)
                                                                                                                                                                                                                                                                                                                                               PRAY/)
                                                                                                                                                                                                                                       FERN/)
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The invention relates to growth factor homologue zvegf4, its corresponding nucleic acid and methods of using them. The sequences of the invention are used in the study and regularion of cell and tissue development, as components of cell culture media and as diagnostic development, as components of cell culture media and as diagnostic skin wounds, including vehous stasis, ulears and other chronic, non-healing wounds, in fracture repair, skin grafting, in constructive cestablish vascular networks in transplanted cells and tissues, or in treating female reproductive tract disorders, including acute or chronic placental insufficiency and prolonged bleeding, it can also be used to promote endothelialisation of vascular grafts and stents, in treating acute or chronic lesions of the gastrointestinal tract or treating or repairing liver damage. Zvegf4 can also be used for treating or corporate competing liver damage. Zvegf4 can also be used for treating hepatic corporate growth and development and demarcate nervous system structures. The control of seases including multiple sclerosis, Alzheimer's disease or parkinson's disease. The polypeptides, mucleic acids and antibodies can also be used to diagnose or treat disorders associated with cell loss or abnormal cell proliferation (including cancer). The cinvention is useful in gene therapy. The present sequence is a fusion corporation is the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New zvegf4 polypeptides and nucleic acids, useful for diagnosing or treating cell loss or abnormal cell proliferation, e.g. cancer, treating full-thickness skin wounds or treating female reproductive tract
                                                                     Growth factor homologue; zvegf4; skin wound; venous stasis; ulcer; fracture repair; skin grafting; neovascularisation; female reproductive tract disorder; bleeding; gastrointestinal tract; liver damage; hepatic chronic passive congestion; CPC; central hemorrhagic necrosis; CHN; neurite growth; neuropathy; neurodegenerative disease; multiple sclerosis; Alzheimer's disease; Parkinson's disease; cell proliferation; cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gilbertson DG;
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                                      Fusion protein #lused in the invention.
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99US-0164463P.
2000US-0180169P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-00564595
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HART/) HART C E.
(SHEP/) SHEPPARD P O.
(GILB/) GILBERTSON D G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gilbert T, Hart CE,
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04-FEB-2000;
                                                                                                                                                                                                                                  Unidentified
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15-APR-2004
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second polypoptages are from 113-136 and residues and compiles.

258-370 amino acid residues of human growth factor homologue ZVEGF4. The protein stimulates proliferation, differentiation, or migration of mesenchymal cells and may modulate activities mediated by cell surface semaphorins. ZVEGF4 may be used to design ant/agonists of neuropilin-semaphorin interactions which may be of use in neurite growth.

5 cardiovascular development, cartilage and limb development. T- and B-cell functions as well as treating rheumatoid arthritis, various forms of cancer, autoimmune diseases, inflammation, retinopathies, haemangiomas, system diseases and peripheral nervow damage, central nervows.

5 cancer, autoimmune disparance in near nerve damage, central nervows.

5 cancer, autoimmune disparance in nerve damage, central nervows.

5 cancer, autoimmune disparance nerve damage, central nervows.

5 cancer, autoimmune paripheral nervous system diseases including stroke.

5 cancer, adminer, diagnostic agents, and research tools and reagents.

5 cancer be used in the study and regulation of cell and tissue development, as components of cell culture media. The proteins can form chomomultimers or heteromultimers that act on tissues to control organ development by modulating cell proliferation, migration, differentiation, development sequence represents a located on chromosome 11q22.3

5 cancer and the control or the specification of claimed but not further defined in the specification)
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190 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGGCGTVNWRSCT
                                                                                                                                                                                                                                                                                                                                                                                                                                   Growth factor homologue; ZVEGF4; proliferation; differentiation; migration; mesenchymal cell; cell surface semaphorin; neuropilin; neurite growth; cardiovascular development; limb development; cartilage development; T-cell; B-cell; rheumatoid arthritis; cancer; autoimmune disease; inflammation; retinopathy; hæmangjoma; ischaemic event; neuropathy; acute nerve damage; stroke; central nervous system disease; peripheral nervous system disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated growth factor analogue ZVEF4 proteins for pharmaceutical
                                                                         61 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR
                                                                                                        250 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR
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                                                                                                                                                                                                                                                                                                                                                                                          ZVEGF4-related fusion protein #2.
                                                                                                                                                                                                                                              ABU72442 standard; protein; 316
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10-NOV-1999; 99US-0164463P.
04-FEB-2000; 2000US-0180169P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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Matches 113; Conservative

Ouery Match Best Local Similarity

100.0%; Score 631; DB 8; Length 302; 100.0%; Pred. No. 8.8e-62; ive 0; Mismatches 0; Indels

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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                 ABG75790;
                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                           ABG75790
                                                                                                                                                                                                                                                                                                                                                                RESULT
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                                                                                                                                                                                                                                                                                                                          DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to growth factor homologue zvegf4, its corresponding nucleic acid and methods of using them. The sequences of the invention are used in the study and regulation of cell and tissue development, as components of cell culture media and as diagnostic agents. The zvegf4 polypeptide can be used in treating full-thickness skin wounds, including venous stasis, ulcers and other thronic, non-healing wounds, in fracture repair, skin grafting, in constructive surgery to promote neovascularisation and increase skin flap survival, to establish vagcular networks in transplanted cells and tissues, or in transplanted cells and tissues, or in transplanted cells and tissues, or in transplanted relations in the construction placental insufficiency and prolonged bleeding. It can also be used to
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                                                                                        204 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFPPRCLLVQRCGGNCGCGTVNWRSCT 263
                                                                          09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New zvegf4 polypeptides and nucleic acids, useful for diagnosing or treating cell loss or abnormal cell proliferation, e.g. cancer, treating full-thickness skin wounds or treating female reproductive tract
                                                                        1 VDLJDRLINDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
                                                                                                                                                                                                                                                                                                             Growth factor homologue, zvegf4, skin wound, venous stasis, ulcer; fracture repair; skin grafting, neovascularisation; female reproductive tract disorder; bleeding, gastrointestinal tract, liver damage, hepartic chronic passive congestion, CPC; central haemorthagic necrosis, CHN; neurite growth; neuropathy; neurodegenerative disease, multiple sclerosis, Alzheimer's disease, Parkinson's disease, cell proliferation; cancer; gene therapy.
                                                 Gaps
                                                                                                                                         264 ÇNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 316
                                                                                                                        61 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 113
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                        Length 316;
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                       Score 631; DB 6;
Pred. No. 9.3e-62;
           100.0%; Sco.
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 55; 73pp; English.
                                                                                                                                                                                                                                                                                      Fusion protein #2used in the invention.
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                                                                                                                                                                                                              ADJ32808 standard, protein, 316 AA.
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99US-0164463P.
2000US-0180169P.
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                                                                                                                                                                                                                                                                (first entry)
                                                 113; Conservative
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SHEPPARD P O.
GILBERTSON D G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hart CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-070738/07
                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GILB/) GILBERT T.
(HART/) HART C E.
 Sequence 316 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         US2004002140-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-NOV-1999;
04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
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                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT 263
promote endothelialisation of vascular grafts and stents, in treating acute or chronic lesions of the gastrointestinal tract or treating or repairing liver damage. Zvegf4 can also be used for treating hepatic chronic passive congestion (CPC) and central haemorrhagic necrosis (CHN). Zvegf4 proteins, agonists and antagonists can also be used to modulate neurite growth and development and demarcate nervous system structures. It can also be used for treating peripheral neuropathies or heurodegenerative disease including multiple sclerosis, Alzheimer's disease or Parkinson's disease. The polypeptides, nucleic acids and antibodies can also be used to diagnose or treat disorders associated with cell loss or abnormal cell proliferation (including cancer). The invention is useful in gene therapy. The present sequence is a fusion protein used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention discloses an isolated human growth factor polynucleotide, designated A.ctg12831-000000.10.0, and the polypeptide it encodes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 631; DB 8;
100.0%; Pred. No. 9.3e-62;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2002; 2002US-00083853.
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Matches 113; Conservative
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Secreted cellular growth factors are molecules which bind to cell surface receptors to regulate a variety of cellular pathways. Growth factors are important in signalling pathways related to embryonic patterning events, cell cycle control, apoptosis, cellular differentiation, cell motility and gene expression. Also disclosed are methods for identifying and gene expression. Also disclosed are methods for identifying condition, or susceptibility to a pathogenic condition, that is associated with a genetic alteration in the growth factor. The growth factor polynucleotide is useful for diagnosing, prognosing or treating (e.g. gene therapy) disorders that are associated with dysfunction of the cyrowth factors, such as developmental and growth disorders, cardiovascular disorders, neurological disorders, metabolic disorders, cancer or immunological diseases. In particular, the polynucleotide is useful for treating or diagnosing e.g. diabetes, osteoporosis, where factors of growth factors. The sequence presented is the human growth factor. A. Ctg12831-000000.10.0, which is disclosed as being encoded by the DNA presented in ABX11387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnerary; VBGF-G; vascular Endothelial Growth Factor; antiatherosclerotic; tumour; proliferatiov; activator; proliferation, differentiation; motility; growth; PDGF-D receptor; antagonist; tissue remodelling; treat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   VDL.DRI_NDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNSGKTVKKYHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 317
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Pred. No. 9.3e-62;
0; Mismatches 0;
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99US-0150604P.
99US-0157108P.
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Heldin C;
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N-PSDB; AAD00737.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                 Sequence 317 AA;
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26-AUG-1999;
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The present sequence is an N-terminally truncated polypeptide of human platelet derived growth factor (PDGP)-D, formally known as Vascular Endothelial Growth Factor (VEGF)-G. It is derived from human foetal lung lambdagt10 cDNA library. It belongs to the VEGF/PDGF family. It functions as an activator of proliferation, differentiation, growth and motility of cells, that express PDGF-D receptor. This sequence is useful for inhibiting the growth of tumours, that express PDGF-D. Expression of PDGF-D and its proteolytic claevage for generating an activated truncated form is useful for regulating receptor binding specificity of PDGF-D. PDGF-D and integonist is useful for inhibiting tissue remodelling during the invasion of tumour cells into normal cells. PGGF-D may be used to treat wounds, atherosclerosis, metastasis and migration of smooth muscle cells
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              Novel polynucleotides encoding a novel growth factor of cells expressing a platelet-derived growth factor, useful for diagnostic and therapeutic applications, e.g. concerning cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antidiabetic; anorectic; cardiant; hypotensive; antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic; neuroprotective; antiparkinsonian; anticonvulsant; osteopathic; antiarthritic; antiinflammatory; dermatological; antiasthmatic; antilipemic, gene therapy; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer; cardiovascular disease; hypertension; atherosclerosis; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder; asthma; dyslipidemia; neurogenesis; inflammatory skin disorder; asthma; dyslipidemia; neurogenesis; cell differentiation; hematopoiesis; wound healing; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFRCLLVQRCGGNCGCGTVNWRSCT
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100.0%; Pred. No. 9.5e-62;
iive 0; Mismatches 0;
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                                                                                                6; 111pp; English.
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2002US-0372019P.
2002US-0374379P.
2002US-0380973P.
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2002US-0370279P.
2002US-0370359P.
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Best Local Similarity 100.
Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 322 AA;
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                                                                                            25; Fig
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12-APR-2002;
22-APR-2002;
15-MAY-2002;
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05-APR-2002;
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Casman S, Bokor JC;
h V, Grosse W, Gunther E;
ll JR, Malyankar UM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alsobrook J, Bento P, Boldog F, Burgess C, Casman S, Bokor JC; Edinger SR, Ellerman K, Fernandes E, Gerlach V, Grosse W, Gunther E Gusev V, Heyes M, Lepley D, Li L, Macdougall JR, Malyankar UM; Millet I, Patturajan M, Peyman JA, Rastelli L, Rieger D, Shenoy S; Shimkets R, Smithson G, Stone D, Vernet C, Voss E;
                  NOVX; human; cardiomyopathy; atherosclerosis; hypertension; pulmonary stenosis; obesity; prostate cancer; diabetes; haemophilia; skin disorder; graft versus host disease; ALDS; asthma; lupus; Crohn's disease; inflammatory bowel disease; ulcerative colitis; multiple sclerosis; infectious disease; anorexia; Alzheimer's disease; Parkinson's disease; NOV4e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polypeptides and nucleic acids, useful for treating or
                                                                                                                                                                                                                                                                                                    01-APR-2002; 2002US-0369065P.
05-APR-2002; 2002US-0370279P.
05-APR-2002; 2002US-037035P.
08-APR-2002; 2002US-03703B1P.
08-APR-2002; 2002US-0370969P.
12-APR-2002; 2002US-037091P.
22-APR-2002; 2002US-0380973P.
15-MAY-2002; 2002US-0380973P.
30-MAY-2002; 2002US-0381329P.
17-JUN-2002; 2002US-0381329P.
17-JUN-2002; 2002US-0381329P.
13-AUG-2002; 2002US-0381329P.
                                                                                                                                                                                                                                                                      31-MAR-2003; 2003US-00403142
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BURGESS C.
CASMAN S.
BOKOR J C.
EDINGER S R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATTURAJAN M.
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RASTELLI L.
RIEGER D.
SHENOY S.
SHIMKETS R.
SMITHSON G.
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GROSSE W.
GUNTHER E.
GUSEV V.
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Gusev V, Heye
Millet I, Pat
Shimkets R, S
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(FERN/)
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(MACD/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MILL/)
    The invention relates to novel NOVX protein and their encoding DNA's, mature forms of the proteins or sequences that are at least 95% identical co, or having one or more conservative amino eaid substitutions in, the proteins. The polypeptides, mucleic acid molecules and antibodies are useful in the manufacture of a medicament for treating a syndrome sesociated with a human disease, preferably a NOVX-associated disorder. The nucleic acid molecules, polypeptides and antibodies are useful for treating, preventing or disgnosing diseases such metabolic disorders. The nucleic acid molecules, polypeptides and antibodies are useful for treating, preventing or disgnosing diseases such metabolic disorders, diabetes, obedity, infectious diseases (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer, cardiovascular diseases (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, epilepsy, immune disorders Alzheimer's costeoarthritis), hematopoiesis, immune disorders as the molecules that also be used as targets for the identification of small molecules that confideration, hematopoiesis, wound healing and anglogenesis, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods. This sequence acids are further used as hybridization probes, in chromosome mapping, the use one of the NOVX proteins of the invention.
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                                                                                                                                                                                                                                                    Stone DJ;
                                                                                                                                                    E, Casman SJ;
Fernandes ER, Gerlach VL;
                                                                                                                                                                                                                                                                                                                                                              New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 113
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                                  17-JUN-2002; 2002US-0389729P.
13-AUG-2002; 2002US-0403491P.
15-AUG-2002; 2002US-0403748P.
31-MAR-2003; 2003US-00403142.
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Matches 113; Conservative
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                                                                                                                                  (CURA-) CURAGEN CORP.
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30-MAY-2002;
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RESULT 20 ADR49109

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This invention describes novel human NOVX polypeptides and the polynucleotides encoding them. The therapeutic is useful in the manufacture of a medicament for treating a syndrome associated with a human disease selected from pathology associated with the polypeptide. Diseases include cardiomyopathy, atherosclerosis, hypertension, pulmonary stenosis, obesity, prostate cancer, diabetes, haemophilia, skin disease, graft versus host disease, AlDS, asthma, lupus, Crohn's disease, inflammatory bowel disease, ulcerative colitis, multiple sachronis, infections disease, anorexia, AlZabaimar's disease, anorexia, PAlZabaimar's disease, chromosome mapping, or tissue typing. This sequence represents the human NOV4e
                    Claim 1; SEQ ID NO 46; 206pp; English.
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US-09-68-2
US-09-723-749-2
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US-09-873-033-2
US-09-468-647A-1101
US-09-468-647A-1101
US-09-468-647A-1102
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US-09-438-046-4

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100.0%; Score 631; DB 4; 100.0%; Pred. No. 4.7e-66; iive 0; Mismatches 0;

Matches 113; Conservative

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Query Match Best Local Similarity

Length 316;

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204 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT 263

61 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 113

1 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT

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100.0%; Pred. No. 4.4e-66;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 55, Application US/09564595D
GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Gilbert, Teresa
APPLICANT: Bart, Charles E.
APPLICANT: Breppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT APPLICATION NUMBER: US 09/304,216
FRIOR APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1990-05-03
PRIOR FILING DATE: 1990-05-03
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
SPRIOR FILING DATE: 1999-11-10
SPRIOR FILING DATE: 1999-11-10
SPRIOR FILING DATE: 1000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                         APPLICANT: Gilbert, Teresa
APPLICANT: Gilbert, Teresa
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT FILING DATE: 200-05-03
CURRENT APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
SEO ID NO 54
LENGTH: 302
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US-09-564-595D-54
; Sequence 54, Application US/09564595D
Patent No. 6495668
; GENERAL INFORMATION:
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Matches 113; Conservative
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US-09-564-595D-55
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264 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 316
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APPLICANT: AASE, Karin
APPLICANT: AASE, Karin
APPLICANT: LEE, Xuri
APPLICANT: LEE, Xuri
APPLICANT: DONTN, Annica
APPLICANT: PONTN, Annica
APPLICANT: OUTELA, Marko
APPLICANT: ALITALO, Kari
APPLICANT: BLING NATE: 1999-11-10
EARLIER APPLICATION NUMBER: 60/107,852
EARLIER FILING DATE: 1999-12-28
EARLIER FILING DATE: 1999-12-28
EARLIER FILING DATE: 1999-08-26
EARLIER FILING DATE: 1999-00-04
EARLIER FILING DATE: 1999-00-04
EARLIER FILING DATE: 1999-10-05
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100.0%; Pred. No. 4.8e-66;
iive 0; Mismatches 0;
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Fatent No. 6432673
GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shepmard, Paul O.
                                                                                                                                                                            Sequence 6, Application US/09438046
Patent No. 6706687
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Best Local Similarity 100.0
Matches 113; Conservative
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                                                                                                                                                                                                               Patent No. 6706687
GENERAL INFORMATION:
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US-09-457-066-37
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US-09-438-046-6
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), OTHER INFORMATION: fusion polypeptide US-09-564-595D-55

TYPE: PRT ORGANISM: Artificial Seguence

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Gaps

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258 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT 317
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                                                                                                                                                                                                                                                                                                                                                                               Length 370;
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APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shemeker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-6001
CURRENT FILING DATE: 2000-11-06
PRIOR APPLICATION NUMBER: US/09/706,968
CURRENT FILING DATE: 2000-11-06
PRIOR APPLICATION NUMBER: US/09/541,752
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 631; DB 4; Best Local Similarity 100.0%; Pred. No. 5.7e-66; Matches 113; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                            PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FASTERQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 37, Application US/09706968
; Patent No. 6528050
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            2000-05-03
                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 113; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
            CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                              US-09-564-595D-2
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LENGTH: 370
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LENGTH: 370
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Best Local Similarity 100.0%; Pred. No. 5.7e-66;
Matches 113; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 631; DB 4; Length 370; 100.0%; Pred. No. 5.7e-66;
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Sequence 2. Application US/09540224

Batent No. 6468543

GENERAL INFORMATION:
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
TITLE OF INVENTION: LICAMENT AND CARTILAGE USING ZVEGF4

FILE REFERENCE: 00-28

CURRENT APPLICATION NUMBER: US/09/540,224

CURRENT FILING DATE: 2000-03-31

EARLIER FILING DATE: 2000-03-31

MUMBER OF SEQ ID NOS: 9

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2

LENTH: 370
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Sequence 2, Application US/09564595D
Fatent No. 6495666
Fatent Application: Growth Factor Homolog ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
APPLICANT: Gilbertgon, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GRÖWTH FACTOR HOMOLOG ZVEGF3;
FILE REPERENCE: 98-60
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT APPLICATION NUMBER: 1999-12-07
NUMBER OF SEQ ID DATE: 1999-12-07
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO3: 50
LENGTH: 370
                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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ORGANISM: Homo sapiens
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US-09-540-224-2
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Best Local Similarity
Matches 113; Conserv
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SEQ ID NO 8
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118 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 370
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APPLICANT: Topouzis, Stavros
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
TITLE OP INVENTION: DISORDERS
FILE REPERENCE: 00-79
CURRENT APPLICATION NUMBER: US/09/808,972
CURRENT APPLICATION NUMBER: US 60/235,295
PRIOR APPLICATION NUMBER: US 60/235,295
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR PILING DATE: 1900-01-03
PRIOR PILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR APPLICATION NUMBER: US 60/132,250
PRIOR PILING DATE: 1999-11-10
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Patent No. 663870
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
TITLE OF INVENTION: LIGAMENT AND CARTILAGE
FILE REFERENCE: 00-12
CURRENT APPLICATION NUMBER: US/09/823,033
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 370
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ORGANISM: Homo sapiens
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US-09-823-033-5
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US-09-438-046-8
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258 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT 317
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100.0%; Score 631; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 5.7e-66;
Matches 113; Conservative 0; Mismatches 0; Indels
Sequence 8, Application US/09438046

Patent No. 6706687

GENERAL INFORMATION:

APPLICANT: ERIKSSON, UIF

APPLICANT: DEXEK KATIN

APPLICANT: DONTN, Annica

APPLICANT: PONTN, Annica

APPLICANT: ALITALO, KATINALO, RATION

APPLICANT: ALITALO, KATINALO, RATION

APPLICANT: OESTHAN, AND

TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, TITLE OF INVENTION: PLATELET-OR AND USES THEREOF

FILE REFERENCE: UIF EXIKSSON et al. 1064-44833

CURRENT APPLICATION NUMBER: US/09/438,046

CURRENT APPLICATION NUMBER: 60/107,852

EARLIER APPLICATION NUMBER: 60/107,852

EARLIER FILING DATE: 1999-11-10

EARLIER FILING DATE: 1999-10-04

EARLIER APPLICATION NUMBER: 60/157,108

EARLIER APPLICATION NUMBER: 60/157,756

EARLIER FILING DATE: 1999-10-05

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PALENTIN VET: 2.0
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APPLICANT: Hart, Charles E.
APPLICANT: Biddington, Christopher S.
APPLICANT: Sheghard, Christopher S.
APPLICANT: Sheghard, Shell O.
APPLICANT: Sheghard, Rimberly E.
APPLICANT: Sheghard, Newly B.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James, Vencor, Debra G.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-60
CURRENT APPLICATION NUMBER: US/10/139,583
CURRENT APPLICATION NUMBER: 09/457,066
PRIOR APPLICATION NUMBER: 09/457,066
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-438-046-8
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CORGANISM: Homo sapiens
US-10-139-583-37
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SEQ ID NO 37
LENGTH: 370
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SEQ ID NO 18
LENGTH: 121
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LENGTH: 200
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Sequence 2, Application US/10039847A

Patent No. 6827938

SEGNERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Topouzis, Stavros
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING
TITLE OF INVENTION: KIDNEY FUNCTION
FILE REFERENCE: 00-100
CURRENT APPLICATION NUMBER: US/10/039,847A
CURRENT FILING DATE: 2002-06-17
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 370
      Length 370;
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100.0%; Score 631; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 5.7e-66;
Matches 113; Conservative 0; Mismatches 0; Indels
                                              Indels
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APPLICANT: ERIKSSON, Ulf
APPLICANT: AAAB, Karin
APPLICANT: LEE, Xuri
APPLICANT: DOTUN, Annica
APPLICANT: PONTN, Annica
APPLICANT: UTTELA, Marko
APPLICANT: ALITALO, Mari
APPLICANT: HELDIN, CARIHERT'S THEREOF
ITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DI
ITLE OF INVENTION: THEREFOR, AND USES THEREOF
ITLE REFERENCE: Ulf Erikason et al 1064-44833
CURRENT APPLICATION NUMBER: US/09/438,046
CURRENT PILING DATE: 1999-11-10
EARLIER FILING DATE: 1999-11-10
EARLIER FILING DATE: 1999-11-10
EARLIER FILING DATE: 1999-12-28
EARLIER APPLICATION NUMBER: 60/107,852
EARLIER FILING DATE: 1999-12-28
EARLIER FILING DATE: 1999-10-26
EARLIER FILING DATE: 1999-08-26
EARLIER FILING DATE: 1999-08-26
EARLIER FILING DATE: 1999-08-26
100.0%; Score 631; DB 4; ilarity 100.0%; Pred. No. 5.7e-66; Conservative 0; Mismatches 0;
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Patent No. 6706687
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ORGANISM: Homo sapiens
Query Match
Best Local Similarity
Matches 113; Conserv
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US-10-039-847A-2
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Sequence 4, Application US/09438046

Patent No. 6706687

GENERAL INFORMATION:

APPLICANT: ELES. Karin

APPLICANT: LEE. Xuri

APPLICANT: DONTW, Anako

APPLICANT: DOSTWA, Anako

APPLICANT: PONTW, Anako

APPLICANT: ALTALO, Kari

APPLICANT: HITCAN, ANAKO

CURRENT PLING DATE: 199-11-10

EARLIER FILING DATE: 199-11-10

EARLIER FILING DATE: 199-11-2-28

EARLIER APPLICATION NUMBER: 60/107,852

EARLIER PILING DATE: 1999-11-30

EARLIER FILING DATE: 1999-11-30

EARLIER PILING DATE: 1999-10-06

MUMBER: FILING DATE: 1999-10-06

MUMBER: FILING DATE: 1999-10-06

MUMBER: FILING DATE: 1999-10-06
                                     60/157,756
EARLIER FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: 60/1
EARLIER FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 97.3<sup>3</sup>
Matches 110; Conservative
                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
US-09-438-046-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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US-10-039-847A-4
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    JS-09-808-972-4
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                                      GENERAL INFORMATION:

APPLICANT: Gilbertson, Debra G.

APPLICANT: Gilbertson, Debra G.

APPLICANT: Hart, Charles E.

TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,

TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4

FILE REFERENCE: 00-28

CURRENT APPLICATION NUMBER: US/09/540,224

CURRENT FILING DATE: 2000-03-31

EARLIER APPLICATION NUMBER: US 60/180,169

EARLIER PILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 9

SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.2%; Score 588; DB 4; Length 370 90.3%; Pred. No. 6.5e-61; ive 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 33, Application US/09564595D
Patent No. 649568
GENERAL INFORMATION:
APPLICANT: Glibert, Teresa
APPLICANT: Glibert, Teresa
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
PRIOR PELICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR PELICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR PELICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 588; DB 4;
Pred. No. 6.5e-61;
6; Mismatches 5
Sequence 4, Application US/09540224
Patent No. 6468543
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Best Local Similarity 90.33
Matches 102; Conservative
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Best Local Similarity 90.33
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Mus musculus
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ORGANISM: Mus musculus
US-09-564-595D-53
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US-09-564-595D-53
                                                                                                                                                                                                                                                                                                   SEQ ID NO 4
LENGTH: 370
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Sequence 4, Application US/10039847A

Patent No. 6827938

GENERAL INFORMATION:

APPLICANT: Hart, Charles E.

APPLICANT: Hart, Charles E.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING

TITLE OF INVENTION: KIDNEY FUNCTION

FILE REFERENCE: 00-100

CURRENT APPLICATION NUMBER: US/10/039,847A

CURRENT FILING DATE: 2002-06-17

PRIOR APPLICATION NUMBER: US 60/244,479

PRIOR FILING DATE: 2002-10-30

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FASELSEQ for Windows Version 3.0
Sequence 4, Application US/09808972

Sequence 4, Application US/09808972

Patent No. 6630142

GENERAL INFORMATION:

APPLICANT: Hart, Charles E.

APPLICANT: TOPOUZIS, Stavros

APPLICANT: TOPOUZIS, Stavros

TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE

TITLE OF INVENTION: DISORDERS

FILE REFERENCE: 00-79

CURRENT APPLICATION NUMBER: US/09/808,972

CURRENT APPLICATION NUMBER: US 60/235,295

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 60/180,169

PRIOR APPLICATION NUMBER: US 60/180,169

PRIOR PILING DATE: 2000-05-04

PRIOR FILING DATE: 1999-11-10

PRIOR FILING DATE: 1999-11-10

PRIOR FILING DATE: 1999-11-10

PRIOR FILING DATE: 1999-105-03

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FASTSEQ FOR WINDOWS Version 3.0
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Best Local Similarity 90.3%; Pred. No. 6.5e-61;
Matches 102; Conservative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.2%; Score 588; DB 4; Length 37 ilarity 90.3%; Pred. No. 6.5e-61; Conservative 6; Mismatches 5; Indels
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Best Local Similarity
Matches 102; Conserv
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35; Indels

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236 VDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQ 295
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                                                                                                                                                                                                                                                                                                                                                           50.7%; Score 320; DB 4; Length 374; 51.3%; Pred. No. 2.2e-29;
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Matches 60; Conservative 14; Mismatches
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PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 60/124,967
PRIOR FILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: US 60/164,131
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 130
SOSTWARE: PATENTIN VERSION 3.2
SEQ ID NO 118
                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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  258 VDLDRLNDDVKRYSCTPRNHSVNLREELKLTNAVFFPRCLLVQRCGGNCGCGTVNWKSCT 317
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                                                                                     61 CNSGKTVKKYHEVLOPEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 113
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                                                                                                                                                                                                                                                                                       GENERAL NO. 8/06847

GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: BRIKSSON, Ulf
APPLICANT: AASE, Karin
APPLICANT: LASE, Xarin
APPLICANT: LASE, Xarin
APPLICANT: BONTN, Annica
APPLICANT: UUTELA, Marko
APPLICANT: OUTELA, Marko
APPLICANT: OLSTMAN, Arne
APPLICANT: ORSTMAN, ARNE
APPLICANT: ORSTMAN, ARNE
FILE REFERENCE: Ulf Eriksson et al 1064-44833
CURRENT FILING DATE: 1999-11-10
EARLIER APPLICATION NUMBER: 60/107,852
EARLIER FILING DATE: 1999-11-10
EARLIER APPLICATION NUMBER: 60/113,997
EARLIER FILING DATE: 1999-10-08
EARLIER FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: 60/157,756
EARLIER PILING DATE: 1999-10-05
NUMBER OF SEO ID NOS: 31
SOFTHARE: PALEALIN VET: 2.0
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APPLICANT: Xu, Jean
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X
FILE REFERENCE: B0192, 70011US00
CURRENT APPLICATION NUMBER: US/09/468,647A
CURRENT FILLING DATE: 1999-12-21
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60.2%; Score 380; DB 4; I
Best Local Similarity 100.0%; Pred. No. 2.3e-37;
Matches 66; Conservative 0; Mismatches 0;
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; Sequence 118, Application US/09468647A
; Patent No. 6783953
; GENERAL INFORMATION:
; APPLICANT: Gordon, Robert D
; APPLICANT: Sprengel, Jorg J
; APPLICANT: Yendel, Jorg J
; APPLICANT: Only Welfery R
; APPLICANT: Onlymans, Josiana J.H.
; APPLICANT: Dijkmans, Josiana J.H.
; APPLICANT: Dijkmans, Josiana J.H.
; APPLICANT: Dijkmans, Josiana J.H.
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                                                                                                                                                                                                                                            Sequence 2, Application US/09438046 Patent No. 6706687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CORGANISM: Homo sapiens
US-09-438-046-2
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SSRPPR 66
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1 VDLDRLNDDAKRYSCTPRNY......DIQLDHHERCDCICSSRPPR 113
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16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
         5.1.6
Compugen Ltd.
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US-10-011-364-6
US-10-31-962-6
US-10-403-142-38
US-11-096-108-4
US-10-271-774-2067
US-10-271-774-2067
US-10-321-962-12
US-009-876-813-54
US-10-877-623-54
US-10-877-623-54
                                                                                                                                                                               hits satisfying chosen parameters:
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          version :
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Maximum Match 100%
Listing first 100 summaries
                                             sw model
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Gapop 10.0 , Gapext 0.5
         GenCore (c) 1993 -
                                             protein search, using
                                                              November 10, 2005,
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length: 2000000000
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Sequence seq

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APPLICANT: Jeffers, Michael
APPLICANT: Shimkets, Richard
APPLICANT: Shimkets, Richard
APPLICANT: Shimkets, Richard
APPLICANT: Shimkets, Richard
APPLICANT: Boldog, Ference
APPLICANT: Burgess, Catherine
APPLICANT: Burgess, Catherine
APPLICANT: Ritnan, B.
APPLICANT: Ritnan, B.
APPLICANT: Shimkets, Juliette
APPLICANT: Shimkets, Juliette
APPLICANT: Labcochelle, William
TITLE OF INVENTION: Factors
TITLE OF INVENTION: Factors
FILE REFERENCE: 1596-557A IBD CIP
CURRENT APPLICATION NUMBER: US/10/011,364
CURRENT FILING DATE: 2001-11-16
PRIOR PELING DATE: 2000-11-06
PRIOR FILING DATE: 2000-11-06
PRIOR FILING DATE: 2001-11-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver: 2.1
LENGTH: 132
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LENGTH: 132
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GENERAL IN CARATION:
APPLICANT: Burgess, Catherine E.
APPLICANT: Burgess, Catherine E.
APPLICANT: Burgess, Elma
APPLICANT: LaRochelle, William J.
APPLICANT: Larochelle, William J.
APPLICANT: Larochelle, William J.
APPLICANT: Peterson, Jeffrey
APPLICANT: Peterson, Jeffrey
APPLICANT: Rittman, Beth
APPLICANT: Rittman, Beth
APPLICANT: Shimkets, Juliette
APPLICANT: Shimkets, Juliette
APPLICANT: Shimkets, Richard A.
APPLICANT: Targen Corporation
APPLICANT: Vang, Meijia Crowth Factors
TITLE OF INVENTION: Using Growth Factors
FILE REPRENCE: 15966-557A IBD CIP2
CURRENT APPLICATION NUMBER: US/10/321,962
CURRENT APPLICATION NUMBER: 2002-12-16
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 6
LENGTH: 132
                                                                     Sequence 6, Application US/10011364; Publication No. US20030153495A1 GENERAL INFORMATION: APPLICANT: Lichenstein, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 6, Application US/10321962; Publication No. US20040006015A1; GENERAL INFORMATION:
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Best Local Similarity
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SGUERAL INFORMATION:

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD FILE REFERENCE: 21402-573A

CURRENT FILING DATE: 2003-03-31

PRIOR APPLICATION NUMBER: 09/569106

PRIOR APPLICATION NUMBER: 09/569106

PRIOR APPLICATION NUMBER: 09/569106

PRIOR PRIOR APPLICATION NUMBER: 09/569106

PRIOR PRIOR APPLICATION NUMBER: 09/569106

PRIOR PRIOR APPLICATION NUMBER: 09/604286

PRIOR PRIOR APPLICATION NUMBER: 09/60206

PRIOR PRIOR DATE: 2000-06-22

PRIOR PRIOR DATE: 2000-06-30

PRIOR PLING DATE: 2000-06-30

PRIOR PLING DATE: 2000-09-30

PRIOR PLING DATE: 2000-09-31

PRIOR PLING DATE: 2000-09-30

PRIOR PRIOR DATE: 2000-09-30

PRIOR PLING DATE: 2000-09-30
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NUMBER OF SEQ ID NOS: 242
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 42
LENGTH: 123
                                      Sequence Seq
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100.0%; Pred. No. 2.8e-61;
ive 0; Mismatches 0;
US-10-125-926A-186
US-10-125-930A-186
US-10-127-831A-186
US-10-127-831B-186
US-10-127-838B-186
US-10-127-843A-186
US-10-127-845A-186
US-10-127-845A-186
US-10-127-845A-186
US-10-127-850A-186
US-10-127-850A-186
US-10-127-850A-186
US-10-127-850A-186
US-10-127-850A-186
US-10-128-684A-186
US-10-128-684A-186
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 113; Conserv
   US-10-403-142-42
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APPLICANT: Herrmann, John
APPLICANT: Boldog, Ferenc
TITLE OF INVENTION: Growth Factor Polypeptides and Nucleic Acids Encoding
TITLE OF INVENTION: Growth Factor Polypeptides and Nucleic Acids Encoding
TITLE OF INVENTION: Growth Factor Polypeptides and Nucleic Acids Encoding
TITLE OF INVENTION: Same
FILE REFERENCE: 15966-577 CON)
CURRENT PAPLICATION NUMBER: US/11/096,308
CURRENT FILING DATE: 2005-04-01
FRIOR APPLICATION NUMBER: USSN 60/158,083
FRIOR APPLICATION NUMBER: USSN 60/188,20
FRIOR PELLING DATE: 2000-03-03
FRIOR PELLING DATE: 2000-03-03
FRIOR PELLING DATE: 1999-10-07
FRIOR APPLICATION NUMBER: USSN 60/189,231
FRIOR APPLICATION NUMBER: USSN 60/159,231
FRIOR APPLICATION NUMBER: USSN 60/159,231
FRIOR APPLICATION NUMBER: USSN 60/174,485
FRIOR APPLICATION NUMBER: USSN 60/123,879
FRIOR FILING DATE: 1999-10-13
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Sequence 2067, Application No. US20040053245A1

Sequence 2067, Application No. US20040053245A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: No. US20040053245A1e1 Nucleic Acids and Polypeptides

TITLE OF INVENTION: NUMBER: US/10/276,774

CURRENT APPLICATION NUMBER: US/200-11-18

PRIOR FILING DATE: 2000-04-18

PRIOR FILING DATE: 2000-04-18

PRIOR FILING DATE: 2000-04-03

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 2700

SOFTWARE: CUSTOM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .; DB 15;
3.5e-61;
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100.0%; Score 631;
Best Local Similarity 100.0%; Pred. No. 3
Matches 113; Conservative 0; Mismatche
                                                        Shimkets, Richard A. Herrmann, John
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US-11-096-308-4
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US-10-276-774-2067
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LENGTH: 152
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TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 2002-573A
CURRENT APPLICATION NUMBER: US/10/403,142
CURRENT FILING DATE: 2003-03-31
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                                                                                                                                                                                                                                                                                                                                                             61 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHBRCDCICSSRPPR 113
                                                                                                                                                                                                                                                                                                                                                                                                  CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHBRCDCICSSRPPR 113
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                                                                                                                       Length 132;
                                                                                                                                                                                   Indels
                                                                                                                                                                                   ö
                                                                                                                       DB 15;
                                                                                                                    Query Match 100.0%; Score 631; DB 15
Best Local Şimilarity 100.0%; Pred. No. 3e-61;
Matches 113; Conservative 0; Mismatches (
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PRIOR FILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
PRIOR PELLING DATE: 2000-04-06
PRIOR PELLING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/36905
PRIOR APPLICATION NUMBER: 09/6026
PRIOR APPLICATION NUMBER: 09/60286
PRIOR APPLICATION NUMBER: 09/61200
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/651200
PRIOR PILING DATE: 2000-09-10
PRIOR APPLICATION NUMBER: 09/688598
PRIOR APPLICATION NUMBER: 09/688598
PRIOR PILING DATE: 2000-10-12
PRIOR PELING DATE: 2001-06-21
PRIOR PELING DATE: 2001-06-21
PRIOR PILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 09/994159
PRIOR PILING DATE: 2001-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-403-142-38
Sequence 38 Application US/10403142
Publication No. US2040162236A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: CuraSequist version 0.1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-321-962+6
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ORGANISM: Homo sapiens
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LENGTH: 132
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US-11-096-308-A
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FILE REFERENCE: 15966-557A IBD CIP2
CURRENT APPLICATION NUMBER: US/10/321,962
CURRENT FILING DATE: 2002-12-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 12
LENGTH: 154
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.(
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-10-321-962-12
                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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APPLICANT: Jeffers, Michael
APPLICANT: Jeffers, Michael
APPLICANT: Jeffers, Richard
APPLICANT: Prayaga, Sudhirdas
APPLICANT: Prayaga, Sudhirdas
APPLICANT: Boldog, Ferenc
APPLICANT: Boldog, Ferenc
APPLICANT: Burgess, Catherine
APPLICANT: Fernandes, Elma
APPLICANT: Fernandes, Elma
APPLICANT: Fernandes, Elma
APPLICANT: Freetment of Inflammatory Bowel Disease Using Growth
TITLE OF INVENTION: Freetment of Inflammatory Bowel Disease Using Growth
TITLE OF INVENTION: Freetment of Inflammatory Bowel Disease Using Growth
TITLE OF INVENTION: Freetment of Inflammatory Bowel Disease Using Growth
TITLE OF INVENTION: Freetment of Inflammatory Bowel Disease Using Growth
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TITLE OF INVENTION: Freetment of Inflammatory Bowel Disease Using Growth
TITLE OF INVENTION: Freetment of Inflammatory Bowel Disease Using Growth
TITLE OF INVENTION UNMER: 09/992, 840
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                                 40 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
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                                                                                                                                                                                       100 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 152
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                                                                                                                                               61 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 113
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APPLICANT: Burgess, Catherine E.
APPLICANT: Pernandes, Elma
APPLICANT: Pernandes, Elma
APPLICANT: Jeffers, Michael E.
APPLICANT: LaRochelle, William J.
APPLICANT: Lichenstein, Henry S.
APPLICANT: Lithenstein, Jeffrey
APPLICANT: Prayaga, Sudhirdas
APPLICANT: Rithman, Beth
APPLICANT: Shimkets, Niliette
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Meijia
APPLICANT: Wang, Meijia
APPLICANT: Curaden Corporation
TITLE OF INVENTION: Treatment of Inflammatory Bowel Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 12, Application US/10321962; Publication No. US20040006015A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 12, Application US/10011364; Publication No. US20030153495A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
US-10-011-364-12
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US-10-011-364-12
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                                                      Gaps
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Query Match 100.0%; Score 631; DB 15; Length 154; Best Local Similarity 100.0%; Pred. No. 3.6e-61; Matches 113; Conservative 0; Mismatches 0; Indels 0;
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US-09-876-813-54

Sequence 54, Application US/09876813

Publication No. US20040002140A1

Sequence 54, Application US/09876813

APPLICANT: Gilbert, Teresa

APPLICANT: Sheppard, Paul O.

TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4

FILE REFERENCE: 99-90-60-60

CURRENT APPLICATION NUMBER: US/09/864,595

PRIOR FILING DATE: 2000-05-03

PRIOR PLING DATE: 2000-05-03

PRIOR FILING DATE: 1999-05-03

PRIOR FILING DATE: 1999-01-10

PRIOR FILING DATE: 1999-01-10

PRIOR FILING DATE: 1999-01-00

PRIOR FILING DATE: 1080-06-04

NUMBER OF SEQ ID NOS: 57

SOFTHARE: PRICE Windows Version 4.0

SEQ ID NO 54

LENGTH: 302
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100.0%; Pred. No. 7.5e-61;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: fusion polypeptide US-09-876-813-54
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y Sequence 54, Application US/10877623
y Publication No. US20040242850A1
GENERAL INFORMATION:
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204 VDLDRLVDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT 263
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; Sequence 2, Application US/10083853
; Publication No. US20020164709A1
; GENERAL INFORMATION:
; APPLICANT: Affwerix, Inc
; APPLICANT: Shigeta, Ron T
; APPLICANT: Shigeta, Ron T
; APPLICANT: Shigeta, Ron T
; PRICANT: Shigeta, Ron T
; TILLE REFERENCE: 3385.1
; CURRENT APPLICATION: NUMBER: US/10/083,853
; CURRENT PILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: USSN 60/272,663
; PRIOR APPLICATION NUMBER: USSN 60/272,663
; RROR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2.
; FROM ARE: Patentin version 3.1
                                                                                                                                                                                                                 264 CNSGKTVKKYHEVLQPEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 31.6
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                                                                                                                                                                    61 CNSGKTVKKYHEVLQFEPGHĮKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hatt, Charles E.
APPLICANT: Hatt, Charles E.
APPLICANT: Abepard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERRNCE: 99-19
CURRENT APPLICATION NUMBER: US/10/877,623
CURRENT FILING DATE: 2004-06-26
PRIOR PLING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 1999-06-03
PRIOR FILING DATE: 1999-06-03
PRIOR FILING DATE: 1999-06-03
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PARLSEQ for Windows Version 4.0
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US-10-877-623-55
; Sequence 55, Application US/10877623
; Publication No. US20040242850A1
; GENERAL INFORMATION;
APPLICANT: Gilbert, Teresa
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APPLICANT: ALIDERL, TELEGRA
APPLICANT: HATC, Charles
APPLICANT: HATC, Charles
APPLICANT: HATC, Charles
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REPERENCE: 99-19
CURRENT FILING DAPE: 2004-06-26
PRIOR PLING DAPE: 2001-06-06
PRIOR PLING DAPE: 2000-05-03
PRIOR PLING DAPE: 2000-05-03
PRIOR PLING DATE: 1999-05-03
PRIOR PLING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR PLING DATE: 1999-11-10
PRIOR PLING DATE: 1999-11-10
PRIOR PLING DATE: 2000-05-03
PRIOR PLING DATE: 1999-11-10
PRIOR PLING DATE: 1999-11-10
PRIOR PLING DATE: 2000-02-04
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Publication No. US20040002140A1
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
ITILE OF INVATION: PROUD GROWTH FACTOR HOMOLOG ZVEGF4
FILE REPERENCE: 99-19
CURRENT FILING DATE: 2001-06-06
PRIOR PPLICATION NUMBER: US/09/564,595
PRIOR FILING DATE: 2000-05-03
PRIOR PPLICATION NUMBER: US 09/304,216
PRIOR PLILING DATE: 1999-05-03
PRIOR PLILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-11-10
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Gaps

Length 316; Indels

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APPLICANT: UUTELA, Marko
APPLICANT: ALITALO, Kari
APPLICANT: ALITALO, Kari
APPLICANT: ALITALO, Kari
APPLICANT: HELDIN, Carl-Henrik
TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES THE PILE REFERENCE: 1064/4833C2
CURRENT APPLICATION NUMBER: US/10/260,539
CURRENT FILING DATE: 2002-10-01
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APPLICANT: ALITALO, MARKA
APPLICANT: ALITALO, Kari
APPLICANT: ALITALO, Kari
APPLICANT: ALITALO, Kari
APPLICANT: ALITALO, Kari
APPLICANT: ALITALO (Ari
APPLICANT: HELDIN, Carl-Henrik
TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES TI
FILE REPERENCE: 1064/44633C2
CURRENT APPLICATION NUMBER: US/10/260,539
PRIOR FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US/10/086,623
PRIOR APPLICATION NUMBER: US/000603-04
PRIOR APPLICATION NUMBER: US/00093-04
PRIOR APPLICATION NUMBER: US/00/9852
PRIOR FILING DATE: 1998-11-10
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                                                                                                                                                                                                                                                                   Sequence 6, Application US/10794392; Publication No. US20050209136A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
                                          AASE, Karin
LI, Xuri
PONTEN, Annica
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APPLICANT: BAIKSSON, Ulf
APPLICANT: AASE, Karin
APPLICANT: LI, Xuri
APPLICANT: PONTEN, Annica
                   APPLICANT: ERIKSSON, Ulf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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APPLICANT:
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APPLICANT: LI, Xurin
APPLICANT: LI, Xurin
APPLICANT: PONTEN, Annica
APPLICANT: UUTELA, Marko
APPLICANT: ALITALO, Karin
APPLICANT: ALITALO, Karin
APPLICANT: HELDIN, Carl-Henrik
TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES TH
FILE REPERENCE: 1064/448332
CURRENT APPLICATION NUMBER: US/10/086, 623
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                                                                               Length 317;
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Pred. No. 8e-61;
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Pred. No. 7.9e-61;
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100.0%; Pred. No. be.
0; Mismatches
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100.0%; Pred. No. ...
0; Mismatches
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PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 60/113,997
PRIOR FILING DATE: 1998-12-28
PRIOR PILING DATE: 1999-08-26
PRIOR PLING DATE: 1999-08-26
PRIOR PLING DATE: 1999-10-04
PRIOR PELING DATE: 1999-10-07
PRIOR APPLICATION NUMBER: US 60/157,108
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-06
PRIOR PLING DATE: 1999-11-06
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-06
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-10
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/10086623
Publication No. US20020164710A1
GENERAL INFORMATION:
APPLICANT: ERIKSSON, U1f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1 SEQ ID NO 6
                                                                               Query Match
Best Local Similarity 100.0
Matches 113; Conservative
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113; Conservative
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-083-853-2
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US-10-086-623-6
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Best Local
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                                      Indels
      100.0%; Pred. No. 8.7e-61;
:ive 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 60/049911
PRIOR PLING DATE: 1997-06-18
PRIOR PLING DATE: 1997-06-18
PRIOR PLING DATE: 1997-08-26
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059117
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-18
PRIOR PLING DATE: 1997-09-19
PRIOR PLING DATE: 1997-00-19
PRIOR PLING DATE: 1997-00-19
PRIOR PLING DATE: 1997-00-17
PRIOR PLING DATE: 1997-00-17
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-24
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Wood, William
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Gurney, Austin L.
Sherwood, Steven
   Best Local Similarity 100.
Matches 113; Conservative
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TITLE OF INVENTION:
FILE REFERENCE:
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US-10-028-072-186
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CURRENT APPLICATION NUMBER: US/69106

PRIOR APPLICATION NUMBER: 09/544511

PRIOR APPLICATION NUMBER: 09/544511

PRIOR PLING DATE: 2000-04-01

PRIOR PAPLICATION NUMBER: 09/604286

PRIOR PLING DATE: 2000-08-10

PRIOR PAPLICATION NUMBER: 09/662783

PRIOR PLING DATE: 2000-09-12

PRIOR PLING DATE: 2000-09-12

PRIOR PELING DATE: 2001-06-21

PRIOR PELING DATE: 2001-09-26

PRIOR PELING DATE: 2001-09-26
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NUMBER OF SEQ ID NOS: 242
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 46
LENGTH: 347
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100.0%; Score 631; DB 18; Length 322;
Best Local Similarity 100.0%; Pred. No. 8e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0
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               PRIOR FILING DATE: 1998-12-28
PRIOR APPLICATION NUMBER: US 60/150,604
PRIOR FILING DATE: 1999-08-26
PRIOR FILING DATE: 1999-10-04
PRIOR FILING DATE: 1999-10-04
PRIOR FILING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: US 60/157,756
PRIOR PILING DATE: 1999-11-0
PRIOR FILING DATE: 1999-11-0
PRIOR FILING DATE: 1999-11-0
PRIOR FILING DATE: 2000-10-19
NUMBER OF SEQ ID NOS: 42
SEQ ID NO 6
LENGTH: 222
PRIOR APPLICATION NUMBER: US 60/113,997
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Publication No. US20040162236A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
US-10-403-142-46
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ORGANISM: Homo sapiens
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	Length 364; Indels 0; Gaps
PRIOR PAPLICATION NUMBER: 60/081818 PRIOR FILING DATE: 1998-04-12 PRIOR FILING DATE: 1998-04-12 PRIOR PILING DATE: 1998-04-23 PRIOR PILING DATE: 1998-04-24 PRIOR PILING DATE: 1998-04-23 PRIOR PILING DATE: 1998-05-07 PRIOR PILING DATE: 1998-05-07 PRIOR PILING DATE: 1998-05-07 PRIOR PILING DATE: 1998-05-13 PRIOR PILING DATE: 1998-05-14 PRIOR PILING DATE: 1998-05-15 PRIOR PILING DATE: 1998-05-16 PRIOR PILING DATE: 1998-05-16 PRIOR PILING DATE: 1998-05-16 PRIOR PILING DATE: 1998-05-17 PRIOR PILING DATE: 1998-05-18	filling DAIE: 1995-07-07-07-07-07-07-07-07-07-07-07-07-07-

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                                       311
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1 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT 60
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APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Anang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACTIOS ENCODING THE SAME
FILE REFERENCE: P3330R1C182
CURRENT APPLICATION NUMBER: US/10/140,808
CURRENT PILING DATE: 2002-05-07
                         252 VDLDRINDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
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                                                                           61 CNSGKTVKKYHEVLQFEPGH1KRRGRAKTMALVDIQLDHHERCDCICSSRPPR 113
112 CNSGKTVKKYHEVLQPEPGH1KRRGRAKTMALVDIQLDHHERCDCICSSRPPR 364
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 186
LENGTH: 364
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Best Local Similarity 100.0%; Pred. No. 9.2e-61;
Matches 113; Conservative 0; Mismatches 0;
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Publication No. US20030022239A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Desnoyers, Luc
APPLICANT: Personovers, Luc
APPLICANT: Pilvaroff, Ellen
                                                                                                                                                                                                                 ; Sequence 186, Application US/10140808; Publication No. US20030017563A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               DeForge Laura
Desnoyers, Luc
All Varoff, Ellen
Gao, Wei-Olang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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US-10-121-049-186
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APPLICANT: Smith, Victoria
APPLICANT: Tumas at Timochy A.
APPLICANT: Tumas at Timochy A.
APPLICANT: Tumas at Timochy A.
APPLICANT: Tumas banie.
APPLICANT: Tumas banie.
APPLICANT: Tanay. Seemin
TITLE OF INVENTION: Seemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE OF SECRETION NUCLEIC SECRETED AND TRANSMEMBRANE OF SECRETION NUCLEIC SERPER 1364;
TITLE OF INVENTION NUMBER: US, 12005, 09:41:03

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vascular endothelial growth factor-related factor 167 N;Alternate names: VRF 167 protein C;Species: Mus musculus (house mouse)
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Best Local Similarity 89.4*
Matches 101, Conservative
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Best Local Similarity
Matches 32; Conserv
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A;Status: preliminary
                                                                                                                                                                                                A; Accession: JC7592
                                                                                                                                                                                                                                                                                                                        A;Gene: scdgf-B
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                                                                                                        Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Species: Homo sapiens
R;Hamada, T.; Ui-Tei, K.; Imaki, J.; Miyata, Y.
B;Hamada, T.; Ui-Tei, K.; Imaki, J.; Miyata, Y.
B;Hamada, T.; Ui-Tei, K.; Imaki, J.; Miyata, Y.
B;Come Biophys. Res. Commun. 280, 733-737, 2001
A;Tile: Molecular cloning of SCDGF-B; a novel growth factor homologous to SCDGF/PDGF-C/A;Reference number: JC7591
A;Molecule type: DNA
A;Residues: 1-370 c+HAM
A;Residues: 1-370 c+HAM
A;Residues: 1-370 c+HAM
A;Residues: UNIPROT:Q9BWV5; UNIPROT:Q9GZP0; DDBJ:AB033832
C;Genetics:
A;Gene: Scdgf-B
F;1-17/Domain: Secretory signal sequence #status predicted cisids
F;18-370/Product: spinal cord-derived growth factor-B #status predicted
F;22-170/Region: COBB domain #status predicted
F;272-370/Region: homologous to platelet-derived growth factor/vascular endothelial grow
F;294-308/Region: conserved motif #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              District derived growth factor-D - mouse
C;Species: Mus musculus (house mouse)
C;Accession: JC7998
B;Zhuo, Y.; Hoyle, G.W.; Zhang, J.; Morris, G.; Lasky, J.A.
Biochem. Biophys. Res. Commun. 308, 126-132, 2003
A;Title: A novel murine PDGP-D splicing variant results in significant differences in pe A;Reference number: JC7998; PMID:12890490
A;Reference number: JC7998
A;Accession: JC7998
A;Molecule type: mRNA
A;Residues: 1-370 < ZHU>
C;Comment: This protein is a potent mesenchymal cell mitogen and chemoattractant involve G;Genetics:
A;Gene: pdgf-D
A;Introns: 42/2; 110/1; 170/2; 191/2; 258/2; 330/1; 334/2
C;Keywords: fibrosis; PDGF-D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.2%; Score 588; DB 2; Length 37/
90.3%; Pred. No. 7.2e-53;
Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 631; DB 2;
Pred. No. 2.7e-57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Scc. No. ...
100.0%; Pred. No. ...
0; Mismatches
ALIGNMENTS
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Matches 113; Conservative
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7592
R;Hamada, T.; Ui-Tei, K.; Imaki, J.; Miyata, Y.
Biochem. Biophys. Res. Commun. 280, 733-737, 2001
A;Title: Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-C/A;Reference number: JC7591; MUID:21092670; PMID:11162582
A;Contents: Fetal brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fil-17/Domain: secretory signal sequence #status predicted <SIG>
Fil-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>
Fig2-170/Region: CUB domain #status predicted
Fig22-370/Region: homologous to plateled-derived growth factor/vascular endothelial grow
Fig24-308/Region: conserved motif #status predicted
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A;Residues: 1-148 cLYT>
A;Cross-references: UNIRROT:B52585; GB:867522; NID:9456900; PIDN:AAB29223.1; PID:9456902
A;Note: sequence extracted from NCBI backbone (NCBIN:141422, NCBIP:141426)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Accession: D49530
R.Lyttle, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J.
Virol. 68, 84-92, 199,
A.Jitle: Homologs of vascular endothelial growth factor are encoded by the poxvirus orf
A.Reference number: A49530; MUID:94076465; PMID:8254780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 VDLDRLNDDVKRYSCTPRNHSVNLRBELKLTNAVFFPRCLLVQRCGGNCGCGTLNWKSCT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CKPRDTVVYLGEEYPESTNLQYNPRCVTVKRCSGCCNGDGQICTAVETRNTTVTVSVTGV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --LORISVIEHTKCDCIGRITTTPIT 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Orf virus
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318 CSSGKTVKKYHEVLKPEPGHFKRRGKAKNMALVDIOLDHHERCDCICSGREPR 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.9%; Score 100.5; DB 2; Length 148; 25.6%; Pred. No. 0.0041; tive 13; Mismatches 31; Indels 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16K vascular endothelial growth factor homolog A2R - Orf virus
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Pred. No. 1.5e-52;
7; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-370 <HAM>
A;Cross-references: UNIPROT:Q9EQT1; DDBJ:AB052170
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.7%;
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precursor

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C;Accession: JS0735
R;Nakahara, K.; Nishimura, H.; Kuro-o, M.; Takewaki, S.; Iwase, M.; Ohkubo, A.; Yazaki, Biochem, Biophys. Res. Comuun. 184, 811-819, 1957
A;Title: Identification of three types of PDGF-A chain gene transcripts in rabbit vascu A;Reference number: JN0248; MUID:92246970; PMID:1575749
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 27-Jun-1994
C;Accession: JN0248
Rivakahara, K.; Nishimura, H.; Kuro-o, M.; Takewaki, S.; Iwase, M.; Ohkubo, A.; Yazaki, B;Ochem. Biophys. Res. Commun. 184, 811-818, 1992
A;Title: Identification of three types of PDGF-A chain gene transcripts in rabbit vascu A;Reference number: JN0248; MUID:92246970; PMID:1575749
A;Reference number: JN0248
A;Molecule type: mRNA
A;Residues: 1-166 <NAX-
C;Superfamily: platelet-derived growth factor
F;1-22/Domain: propeptide (fragment) #status predicted <PRO>
F;23-166/Product: platelet-derived growth factor A3 chain #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A)Cross-references: UNIPROT:P94007
A;Note: this protein corresponds to the endothelial type of human A chain C;Superfamily: platelet-derived growth factors
F;1-20/Domain: signal sequence Hetatus predicted <SIG>F;21-89/Domain: propeptide #status predicted <PRO>F;21-89/Domain: propeptide #status predicted <PRO>F;90-198/Product: platelet-derived growth factor Al chain #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 ANFLIMPPCVEVKRCTGCC----NTSSVKCOPSRVHHRSVKVAKVE--YVRKKPKKE- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEGF-C, is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        platelet-derived growth factor chain Al precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 09-Oct_1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 ANVVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGH1KRRGRAKTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 ANVVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 166,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 94; DB 2; Length 198; Pred. No. 0.025; 17; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            14.9%; Score 94; DB 2; Le 28.0%; Pred. No. 0.021; ive 17; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: nucleic acid sequence not shown A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 --VQVRLEEHLECACAASSAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --VQVRLEEHLECACAASSAGP
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28.0%;
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Best Local Similarity 28.0%
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Best Local Similarity
Matches 23; Conserv
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C;Species: Mus musculus (house mouse)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: JG-679
R;TOwnson, S:; Lagercrantz, J:; Grimmond, S.; Silins, G.; Nordenskjoeld, M.; Weber, G.;
Biochem. Biophys. Res. Commun. 220, 922-928, 1996
A;Title: Characterization of the murine VEGF-related factor gene.
A;Reference number: JG-679; MUID:96183052; PMID:8607868
A;Accession: JG-679
A;Mollecule type: mRNA
A;Residues: 1-207 < TOWA
A;Residues: 1-207 < TOWA
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C;Comment: This factor is a mitogen, that is selective for endothelial cells, and belong larger endothelial growth factors 167 and 186.
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: JC4680
R;Townson, S: Lagercrantz, J:; Grimmond, S:; Silins, G:; Nordenskjoeld, M.; Weber, G:;
Blochem. Biophys. Res. Commun. 220, 922-928, 1996
A;Title: Characterization of the murine VEGF-related factor gene.
A;Reference number: JC4679; MUID:96183052; PMID:8607868
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A;Residues: 1-188 < TOW>
A;Residues: 1-188 < TOW>
A;Cross-references: UNIPROT: P49766; GB:U43837; NID:g1314335; PIDN:AAC52553.1; PID:g13143
C;Comment: Thig factor is a mitogen, that is selective for endothelial cells, and belong C;Genetics:
A;Gene: vrf
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A,Map position: 19
C;Keywords: growth factor
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-207/Product: vascular endothelial growth factor related factor #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Map position: 19
A,Introns: 137/2
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-188/Product: vagcular endothelial growth factor-related factor #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 RATCQPREVVVPLSMEL-MGNVVKQLVPSCVTVQRCG---GCCPDDGLECVPTGQHQVRM 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vascular endothelial growth factor-related factor 186 precursor - mouse N;Alternate names: VRF 186 protein, VEGF 186 C;Species: Mus musculus (house mouse) C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004 C;Accession: JC4679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 RATCQPREVVVPLSMEL-MGNVVKQLVPSCVTVQRCG---GCCPDDGLECVPTGQHQVRM
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C;Species: Oryctolagus cuniculus (domestic rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 15.1%; Score 95.5; DB 2; Length 188; Similarity 27.9%; Pred. No. 0.017; 29; Conservative 16; Mismatches 38; Indels 2
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Best Local Similarity 27.9%; Pred. No. 0.018;
Matches 29; Conservative 16; Mismatches 38; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 YHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 QILMIQY-----PSSQLGEMSLEEHSQCEC----RPKK 128
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Matches 2
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A;Molecule type: mRNA
A;Reaidues: 1-196 <MER>
A;Cross-rcoss: G3:Mg29464
C;Superfamily: platelet-derived growth factor
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Matches 22; Conserv
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A;Residues: 1~196 <BON>
                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                              Query Match
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A;Residues: 1-419 c,000-
A;Residues: 1-419 c,000-
A;Residues: 1-419 c,000-
A;Rote: null Pull:RPCT:P49767; EMBL:X94216; NID:g1177488; PIDN:CAA63907.1; PID:e221
A;Rote: null Pull: A part of the translation is shown
A;Rote: null Pull: A part of the translation is shown
A;Rote: null Pull: Pull: A part of the translation is shown
A;Rote: null Pull: A part of the translation is shown
A;Rote: null Pull: A part of the translation is shown
A;Rote: nulled: a revision to the sequence from reference S61795
R;Goldov, V.; Pajusola: K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kuk, E.; Saksela,
EMBO U. 15, 290-298 1996
A;Reterence number: S61795; MUD:9617824; PMID:8617204
A;Reterence number: S61795; MUD:9617824; PMID:8617204
A;Rocessidue: 70-419 c,001
A;Rocessidue: 70-419
A;Rocessi
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Dataclet-derived growth factor chain A precursor - mouse
Dataclet-derived growth factor chain A precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 07-May-1999
C;Accession: A37359
C;Accession: A37359
Dev. Biol. 138, 114-122, 1990
A;Title: Selective expression of PDGF A and its receptor during early mouse embryogenesi
A;Reference number: A37359; MUID:90169294; PMID:2155144
A;Reference number: A37359
A;Reference number: A37359
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Matches 38; Conservative
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platelet-derived growth factor chain A precursor (version 2) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C;Accession: A40851; I51891
R;Katayose, D.; Ohe, M.; Yamauchi, K.; Ogata, M.; Shirato, K.; Fujita, H.; Shibahara, S.
A;Title: Increased expression of POGF A- and B-chain genes in rat lungs with hypoxic pul
A;Reference number: A40851; MUID:93191115; PMID:8447423
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F.
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R;Bonthron, D.; Collins, T.; Grzeschik, K.H.; van Roy, N.; Speleman, F.
Genomics 13, 257-263, 1992
A;Title: Platelet-derived growth factor A chain: confirmation of localization of PDGFA 1
A;Reference number: A42002; MUID:92307656; PMID:1612586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               platelet-derived growth factor chain A precursor splice form 2 - human C; Species: Homo sapiens (man)
C; Date: 30-Un-1999 #sequence revision 30-Jun-1989 #text_change 09-Jul-2004
C; Accession: B28964; B42002; B28122
R; Bonthron, D.T.; Morton, C.C.; Orkin, S.H.; Collins, T.
Proc. Natl. Acad. Sci. U.S.A. 85, 1492-1496, 1988
A; Title: Platelet-derived growth factor A chain: gene structure, chromosomal location, A; Reference number: A28964; MUID:88144463; PMID:3422746
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A,Molacule type: mRNA
A,Residues: 1-196 «KAT>
A,Cross-references: GB:D10106; NID:g220839; PIDN:BAA00987.1; PID:g220840
A,Experimental source: brain
A,Nove: sequence extracted from NCBI backbone (NCBIP:126515)
C,Superfamily: platelet-derived growth factor
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R;Residues: F; Bywater, M.; Knott, T.J.; Scott, J.; Betsholtz, C. Mol. Cell. Biol. 8, 571-577, 1988
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                                                         Indels
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DB 2;
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                            0.081;
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                                                         18; Mismatches
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Score 89;
Pred. No.
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14.1%;
26.8%;
                                                         22; Conservative
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R;Bonthron, D.T.; Morton, C.C.; Orkin, S.H.; Collins, T.

Proc., Natl. Acad. Sci. U.S.A. 85, 1492-1496, 1988
A;Title: Platelet-derived growth factor A chain: gene structure, chromosomal location, e. A;Reference number: A28964; MUID:88144463; PMID:3422746
A;Accession: A28964
A;Molecule type: DNA
A;Rodecule type: DNA
A;Rossidues: 1-211 & BON>
A;Cross-references: UNIPROT:P04085; GB:M21571; GB:J03638; GB:M19984; GB:M19985; GB:M1999*
B;Cross-references: UNIPROT: 511-514, 1994
B;Cohim. Biophys. Acta 1222, 511-514, 1994
A;Title: Gene regulation by the 5'-untranslated region of the platelet-derived growth factor number: S47564; MUID:94312450; PMID:7518695
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R;Bonthron, D.; Collins, T.; Grzeschik, K.H.; van Roy, N.; Speleman, F.
Renomics 13, 257-263, 1992
A;Title: Platelet-derived growth factor A chain: confirmation of localization of PDGFA A;Reference number: A42002; MUID:92307656; PMID:1612586
A;Accession: A42002
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26.8%;
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Best Local Similarity
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-21 < TAK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Description: Cross-species conservation in sequence and function of PDGF ligands and marked centenumber: $25096
A; Accession: $25096
A; A; Residues: 1-197 *HER1>
A; Residues: 1-197 *HER1>
A; Residues: 1-197 *HER1>
A; Residues: UNIPNOT: P28576; EMBL: Z14120; NID: 956865; PIDN: CAA78490.1; PID: 956866
B; Herren. B: Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.
A; Title: Conservation in sequence and affinity of human and rodent PDGF ligands and rece A; Accession: $33764; MUID: 93305723; PMID: 8318539
A; Accession: $33764
A; Molecule type: mRNA
A; Residues: 89-172 *HER2>
A; Cross-references: EMBL: Z14120
C; Superfamily: platelet-derived growth factor
C; Superfamily: platelet-derived growth factor
Title: Structural characterization of the human platelet-derived growth factor A-chain
Reference number: A28122; MUID:88174698; PMID:2832727
                                                                                                                                                                                                                 .Note: the authors translated the codon ACA for residue 64 as Arg, CGT for residue 65 a
.Comment: Exon 6 is spliced out of this variant splice form. For the major splice form
.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Rattus norvegicus (Norway rat)
C; Date: O'7-Apr-1994 #sequence_revision O'7-Apr-1994 #text_change 09-Jul-2004
C; Accession: S25096; S33764
R; Herren, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.
R; Herren, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.
A; Herren, B.; Meyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.
A; Herren, B.; Meyer, B.; Meyer, M.; Loetscher, P.; Pech, M.
A; Reference number: S25096
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                                                                A; Accession: B28122
A; Molecule type: mRNA
A; Residues: 1-63, 'TRD', 67-196 <ROR>
A; Residues: 1-63, 'TRD', 67-196 <ROR>
A; Cross-references: GB:M2048
A; Mote: the authors translated the codon ACA for residue 64 as Arg, CGT for residue C; Comment: Exon 6 is spliced out of this variant splice form. For the major splic C; Genetics:
A; Gene: GB:PDGFA
A; Cross-references: GB:120266; OMIM:173430
A; Cross-references: GB:120266; OMIM:173430
C; Superfamily: platelet-derived growth factor
C; Superfamily: platelet-derived growth factor
C; Keywords: alternative splicing; glycoprotein; growth factor; mitogen; platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 ANFLIWPPCVEVKRCTGCC----NTSSVKCOPSRVHHRSVKVAKVE--YVRKKPKLKE- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 ANVVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTM 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              latelet-derived growth factor chain A precursor - rat (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 14.1%; Score 89; DB 2; I. Similarity 26.8%; Pred. No. 0.081; 22; Conservative 18; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --VQVRLEEHLECACATTSLNP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 -- VQVRLEEHLECACATSNLNP 179
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Best Local Similarity
Matches 22; Conserva
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A; Molecule type: mRNA
A; Residues: 1-211 < BBT>
A; Cross-references: GB:X03795; NID:g35365; PIDN:CAA27421.1; PID:g35366
A; Experimental source: clonal glioma cell line U-343 MGaCl2:6, a tumor cell line
R; Hoppe, J.; Schumacher, L.; Eichner, W.; Weich, H.A.
R; Hoppe, J.; Summacher, L.; Eichner, W.; Weich, H.A.
A; Title: The long 3' untranslated regions of the PDGF-A and -B mRNAs are only distantly
A; Reference number: S00173; MUID:88030061; PMID:3666150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Molecule type: mRNA
A, Residues: 1-193,'DVR' <HOP>
A, Residues: 1-193,'DVR' <HOP>
A, Residues: 1-193,'DVR' <HOP>
A, Residues: 1-193,'DVR' <HOP>
A, Rossidues: 1-193,'DVR' <HOP>
B, Rossidues: 1-193,'DVR' <HOP>
B, Rossidues: 1-193,'DVR' <HOPL' T.J.; Scott, J.; Betsholtz, C.
Mol. Cell. Biol. 8, S71-577, 1988
A, Title: Structural characterization of the human platelet-derived growth factor A-chair A, Reference number: A28122; MUID:88174698; PMID:2832727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Molecule type: mRNA
A.Residues: 1-63, TRD', 67-211 <ROR>
A.Residues: 1-63, TRD', 67-211 <ROR>
A.Residues: 1-63, TRD', 67-211 <ROR>
A.Cross-references: GB:MO1488
A.Note: the authors translated the codon ACA for residue 64 as Arg, CGT for residue 65 C;Comment: Platelet-derived growth factor, a potent mitogen for cells of mesenchymal or C;Comment: A carboxyl-terminal propeptide may be removed from the precursor by proteoly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Fourier 1922-1922
A, Fourier 1922-1922
A, Fourier 1922-1922
A, Map position: 7922-792
A, Map position: 7922-792
A, Map position: 7922-792
A, Map position: 7922-792
A, Map position: 24/3; 84/1; 84/1; 151/3; 194/1
C, Complex: homodimer; heterodimer (see PIR. PFHUG2)
C, Superfamily: platelet-derived growth factor
C, Keywords: alternative splicing; glycoprotein; growth factor; mitogen; platelet
C, Keywords: alternative splicing; glycoprotein; growth factor; mitogen; platelet
F; 1-20/Domain: signal sequence #status predicted < RGO
F; 21-86/Domain: propeptide #status predicted < RRO>
F; 21-87 Region: receptor binding #status predicted
F; 87-211/Product: platelet-derived growth factor chain A #status predicted
F; 87-211/Product: platelet-derived growth factor chain B-133 in heterodimeric form) #status predicted
F; 123/Disulfide bonds: interchain (to chain B-133 in heterodimeric form) #status predicted
F; 132/Disulfide bonds: interchain (to chain B-124 in heterodimeric form) #status predicted
F; 134/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Score 89; DB 1; Length 211; Pred. No. 0.087;

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platelet-derived growth factor a chain short of the chain short of the chain short of the chain clawed frog)

C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C; Accession: 15151
R; Mercola, M; Melton, D.A.; Stiles, C.D.
Scherce 24, 1223-1225, 1988
A; Title: Platelet-derived growth factor A chain is maternally encoded in Xenopus embryos A; Reference number: 151550; MUID:88321676; PMID:3413486
A; Accession: 151551
A; Accession: E1555
A; Accession: E1555
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-200 «MER>
A;Cross-references: UNIPROT:P13698; GB:M23238; NID:g214650; PIDN:AAA49928.1; PID:g214651
C;Superfamily: platelet-derived growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: $08220
K;Bejcek, B.E.; Li, D.Y.; Devel, T.F.
Nucleic Acids Res. 18, 680, 1990
A;Title: Nucleotide sequence of a cDNA clone of Xenopus platelet-derived growth factor A
A;Reference number: $08220; MUID:90175018; PMID:2308861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-215 <BEJ>
A; Roost-references: UNIPOT: P13698; EMBL:X17545; NID:g64973; PIDN:CAA35583.1; PID:g64974
C; Superfamily: platelet-derived growth factor
C; Keywords: alternative splicing; growth factor
C; Keywords: alternative splicing; prowth factor
C; Keywords: alternative splicing; prowth factor
C; F1-22/Domain: propeptide #status predicted <RIG>
F; 21-29/Domain: propeptide #status predicted <PRO>
F; 22-215/Product: platelet-derived growth factor chain A #status predicted <MAT>
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C;Species: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: 151550
C;Accession: 151550
Skimercola, M.; Meltoon, D.A.; Stiles, C.D.
Science 241, 1223-1225, 1988
A;Title: Platelet-derived growth factor A chain is maternally encoded in Xenopus embryos.
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 ANVVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTM
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0.34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.2%; Score 83; DB:
ilarity 26.6%; Pred. No. 0.36
Conservative 18; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --VLVRLEEHLECTCTANS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 ALVDIQLDHHERCDCICSS 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Accession: S08220
A, Status: translation not shown
A, Molecule type: mRNA
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Matches 21; Conserv
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Matches 21; Conserv
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Cispecies
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T03404

metallothionein-like protein - rice
metallothionein-like protein - rice
metallothionein-like protein - rice
metallothionein-like protein - rice
c;Species: Oryza sativa (rice)
c;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03404
R;Yu, L.H.; Umeda, M.; Liu, J.Y.; Zhao, N.M.; Uchimiya, H.
R;Yu, L.H.; Umeda, M.; Liu, J.Y.; Zhao, N.M.; Uchimiya, H.
R;Yu, L.H.; Umeda, M.; Liu, J.Y.; Zhao, N.M.; Uchimiya, H.
R;Yu, L.H.; Umeda, M.; Liu, J.Y.; Zhao, N.M.; Uchimiya, H.
R;Yu, L.H.; Umeda, M.; Liu, J.Y.; Zhao, N.M.; Uchimiya, H.
R;Title: A novel MT gene of rice plants is strongly expressed in the node portion of A;Title: A novel MT gene of rice plants is strongly expressed in the node portion of A;Accession: T03404
A;Accession: T03404
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 180 cyUL>
A;Molecule type: mRNA
A;Residues: 180 cyUL>
A;Accession: Umb:g1944204; PIDN:BAA19661.1; EC;Superfamily: metallothionein
а
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32;
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Pred. No. 0.13;
2; Mismatches 7;
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A,Reference number: 151550, MUID:88321676; PMID:3413486
A;Accession: 151550
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residugs: 1-226 <MER>
A;Cross-references: UNIPROT:P13698; GB:M23237; NID:g214648; PIDN:AAA49927.1; PID:g214649
C;Superfamily: platelet-derived growth factor
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12.5%; Score 79; DB 1; Length 241;
Best Local Similarity 30.1%; Pred. No. 1;
Matches 25; Conservative 12; Mismatches 34; Indels
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13.2%; Score 83; DB 2; Length 226;
Best Local Similarity 26.6%; Pred. No. 0.38;
Matches 21; Conservative 18; Mismatches 30; Indels
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2: uniprot_trembl:*
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Altausher R.D. Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jorden H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brahles S., Logdelland N.P., Peters G.J., Abramson R.D., Mullahy S.J.,

Rahle S.S., Logdellando N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rahle S.S., Logdellando N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rahles S.S., McEwan P.J., McKernan K.J., Malek J.A., Gluba R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffaxd G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Richards M., Marra M.A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                   Wistow G., Berstein S.L., Ray S., Wyatt M.K., Behal A., Touchman J.W., Bouffard G., Smith D., Peterson K.; "Expressed sequence tag analysis of adult human iris for the NEIBank Project: steroid-response factors and similarities with retinal pigment epithelium."; Mol. Vision 8:185-195(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Roster J., Grimandi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singhon J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."

Genome Res. 13:2265-2270(2003).

EMBL, AN207518, AAX20082.1; -.

EMBL, BC030645; AAX30645.1; -.

EMBL, AN359116; AAQ89474.1; -.
                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                        01-UNA-2001 (TrEMBLrel. 17, Created)
01-UNA-2001 (TrEMBLrel. 17, Last sequence update)
25-OCT-2004 (TrEMBLrel. 18, Last annotation update)
1ris-expressed growth factor short form (Platelet derived growth factor D, isoform 2) (SCDGF-B).

Name=IEGF; Synonyms=PDGFD; ORFNames=UNQ1899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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                                                         364 AA.
                                                                                                                                                                                                                                                                                                                                              TISSUE=1ris;
MEDLINE=22103462; Pubmed=12107412;
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                                                         PRELIMINARY;
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Godowski P.;
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                 RESULT 1
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Spinal cord-derived growth factor-B (MSTP036) (Platelet-derived growth factor 10) (Iris-expressed growth factor long form).
Name=hSCDGF-B; Synonyms=IEGF, PDGFD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVPFPRCLLVQRCGGNCGCGTVNWRSCT
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MEDLINE=21092670; PubMed=11162582; DOI=10.1006/bbrc.2000.4187;
Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
"Molecular cloning of SCOFF-B, a novel growth factor homologous to SCDGF/PDGF-C/fallotein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 113
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LaRochelle W.J., Joffers M., McDonald W.F., Chillakuru R.A.,
Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Ver
Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets
Shimkets R.A., Rothborrg J.M., Lichenstein H.S.;
"PDGF D, A Novel Procease-Activated Growth Factor.";
Nat. Cell Biol. 3:517-521(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 364;
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HSSP, OSJUSB; INTO:

GO; GO:0016020; C:membrane; IEA.

GO; GO:0008031; F:growth factor activity; IEA.

GO; GO:0008121; P:cell growth and/or maintenance; IEA.

InterPro; IPR000859; CUB.
InterPro; IPR000072; PD growth factor.

InterPro; IPR000072; PD growth factor.

InterPro; IPR000072; PD growth factor.

PEOSITE; PS01180; CUB; 1.

PROSITE; PS01180; CUB; 1.

PROSITE; PS0278; PDGF 2; 1.

PROSITE; PS0430; TONB DEPENDENT REC 1; UNKNOWN 1.

SEQUENCE 364 AA; 42166 MW; 245C53E8DDEA9EAC_CRC64;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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; Pred. No. 3.6e-61;
0; Mismatches 0;
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Nat. Cell Biol. 3:512-516(2001).
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Best Local Similarity 100.
Matches 113; Conservative
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SEQUENCE FROM N.A.
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                                                                                Wistow G., Berstein S.L., Ray S., Wyatt M.K., Behal A., Touchman J.W., Bouffard G., Smith D., Peterson K.;

Bouffard G., Smith D., Peterson K.;

"Expressed sequence tag analysis of adult human iris for the NEIBank Project: steroid-response factors and similarities with retinal pigment epithelium.";

Mol. Vision 8:185-195(2002).

EMBL, AB033823, BAB189321;

EMBL, AF112216; AAG392971;

EMBL, AF335584; AAK388401;
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    092517; Q9D118; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 27, Last annotation update) Platelet-derived growth factor D (Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110003109 product:platelet-derived growth factor D).
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STRAIN=BALB/C;
BADINES_21231380; PubMed=11331882; DOI=10.1038/35074593;
LaRochelle W.J., Jeffers M., McDonald W.F., Chillakuru R.A., Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet Burgess C.E., Pernandez E., Deegler L.L., Rittman B., Shimkets J., Shimket B. A. Rochberg J.M., Lichenstein H.S.;
"PDGF D, A Novel Protease-Activated Growth Factor.",
Nat. Cell Biol. 3:517-521(2001).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0008083; F:growth factor activity; IEA.
GO; GO:0008151; P:cell growth and/or maintenance; IEA.
GO:GO:0008151; P:cell growth and/or maintenance; IEA.
InterPro; IPR000859; CUB.
InterPro; IPR00012; PD growth factor.
InterPro; IPR00131; CUB; 1.
SMART; SM00141; PDGF; 1.
RPOSITE; PS01180; CUB; 1.
RPOSITE; PS01180; CUB; 1.
RPOSITE; PS0130; TONB DEPENDENT REC 1; UNKNOWN 1.
SEQUENCE 370 AA; 42848 MW; D387F485E7BB7674*CRC64;
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                                                                 MEDLINE=22103462; PubMed=12107412;
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Matches 113; Conservative
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STRAIN-CSTBL/60; TISSUB-Whole body;

STRAIN-CSTBL/60; TISSUB-Whole body;

Adachi J., Alzawa K., Akahira S., Akimura T., Arai A., Aono H.,

Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

A managaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

A kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

A kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

A cokazaki Y., Okido T., Owa C., Salto H., Saito R., Sakai K.,

Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

Sogabe Y., Cova T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

A Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

BMBL, AR335583; AAK3883991; ---

BRBL, AK003359; BAR22735.2; ---

REMBL, AK003359; ANK3883991; ---

REMBL, AK00359; ANK3883991; ---

REMBL, AK003359; ANK388391; ---

REMBL, AK003359; ANK3883991; ---

REMBL, AK003359; ANK3883991; ---

REMBL, AK003359; ANK3883991; ---

REMBL, AK00359359; ANK3883991; ---

REMBL, AK003593; ANK3883991
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MGD; MGI1919052; PdGfd.

GO: GO: 0005615; C:extracellular space; TAS.

GO; GO: 0005615; C:extracellular space; TAS.

GO; GO: 0005615; C:extracellular space; TAS.

GO; GO: 00050730; P:regulation of peptidyl-tyrosine phosphoryla. . .; IDA.

FRAM; PRO421; CUB; 1.

SMART; SM00042; CUB; 1.

SMART; SM0141; PDGF; 1.

*PROSITE; PS01180; CUB; 1.

*PROSITE; PS0278; PDGF_2; 1.

*PROSITE; PS50278; PDGF_2; 1.
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SEQUENCE FROM N.A.
STRAIN-C57BJ/6J; TISSUE=Whole body;
Garnin-C57BJ/6J; TISSUE=Whole body;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Garninci P., Shibata Y., Hayatau N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Cormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=110.1757-1771(2000);

MEDLINE=20530913; PubMed=110.152600;

MEDLINE=20530913; PubMed=110.1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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STRAIN-C57BL/6J; TISSUE-Whole body;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II
                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Whole body;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                     cDNA cloning.";
Carninci P., Hayashizaki Y., "High-efficiency full-length c
Meth. Enzymol. 303:19-44(1999)
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Best Local Similarity 90.3
Matches 102; Conservative
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Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                      300 AA; 34616 MW; 716C873C9C01C0C6 CRC64;
         MEMBL, AV37260; AAQ24932.1; --
GO, GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:000803; F:growth factor activity; IEA.
GO; GO:0008151; P:cell growth and/or maintenance; IEA.
InterPro; IPR000859; CUB.
InterPro; IPR000072; PD_growth_factor.
Fram: PF00411; CUB; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01180; CUB; 1.
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Matches 91; Conservative
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                  258 VDLDRLNDDVKRYSCTPRNHSVNLKEELKLTNAVFFPRCLLVQRCGGNCGCGTVNWKSCT 317
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1 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT 60
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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MEDLINE=21092670; Pubmed=11162582; DOI=10.1006/bbrc.2000.4187;
Mamada T., Ui-Fer K., Imaki J., Miyata Y.;
"Molecular cloning of SCOFF-B, a novel growth factor homologous to SCOGF/PDGF-C/fallotein.";
                                                                                        61 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 113
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PROSITE; PS50278; PDGF 2; 1.
CROHENCE 370 AA; 42809 MW; 7BE8A251F679BF73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR 2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Spinal-cord derived growth factor-B.
Name=rSCDGF-B,
Rattus norvegicus (Rat).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Iris-expressed growth factor (Fragment).
                                                                                                                                                                                                 370 AA
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Q6V9H4;
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                                                                                          202 VDLDRLNDDAKRYSCTPRNYSVNLREELKLTNVVFFPRCLLVQRCGGNCGCGTVNWKSCT 261
                                                                         9
                                                                         1 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVORCGGNCGCGTVNWRSCT
                                       Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li X., Ponten A., Aase K., Karlsson L., Abramsson A., Uutela M., Backtrom G., Hellstrom M., Bostrom P., Li H., Soriano P., Bersholtz C., Heldin C.-H., Alitalo K., Ostman A., Eriksson U., "PDGF-C is a new protease-activated ligand for the PDGF alpha-
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Nat. Cell Biol. 2:302-309(2000).
-!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
EMBL; APZ4813; APR80597.1; -.
HSSP; Q9JJS8; 1NTO.
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81.0%; Score 511; DB 2; Length 300; 91.9%; Pred. No. 5.1e-48; ive 4; Mismatches 4; Indels
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MEDLINE=20268201; PubMed=10806482; DOI=10.1038/35010579;
Tesni L.. Abramsson A., Uv
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                                                                                                                                                                  61 CNSGKTVKKYHEVLQFEPGHIKRRRRRKTMALVDIQLDH 99
                                                                                                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Platelet-derived growth factor C.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 50.5%; Score 318.5; DB 2; Best Local Similarity 53.3%; Pred. No. 1e-26; Matches 57; Conservative 14; Mismatches 33;
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0008083; F:growth factor activity; IEA.
GO; GO:0008283; P:cell proliferation; IEA.
GO; GO:000074; P:regulation of cell cycle; IEA.
                                                                                                                                                                                                                                                                             345 AA
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InterPro, IPR000072; PD_growth_factor
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PROSITE; PS50278; PDGF_2; 1.
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SEQUENCE 345 AA; 390
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Oryctolagus cuniculus (Rabbit). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.

SEQUENCE FROM N.A. S., Wistow G.;

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NCBI_TaxID=9986;

Name=PDGFD;

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InterPro; IPR000072; PD_growth_factor
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Q91946;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21347863; PubMed=11297552; DOI=10.1074/jbc.M101056200;
Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O.,
Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M.,
Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.;
"Platejet-derived growth factor C (PDGF-C), a novel growth factor that binds to PDGF alpha and beta receptor.";
1 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Godowski P.;
"The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."
Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20461776; PubMed=11004490; DOI=10.1016/S0167-4781(00)00066-X;
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"Identification of a novel platelet-derived growth factor-like gene, fallotein, in the human reproductive tract.";
Biophys. Acta 1492:196-202(2000).
                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Secretory growth factor-like protein fallotein (Spinal cord-derived
growth factor) (Platelet-derived growth factor C) (VEGF-E).
Name-hSCDGF; Synonyms-PDGFC; ORFNames-UNQ174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Curney A.L., Abaya E., Baker K., Baldwin D., Brush J., Clen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P. Eaton D., Roster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Leino D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watenabe C., Wieand D., Woods K., Xie M.H., Yansuxa D., Yi S., Yu G., Yuen J., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                      CNSGKTVKKYHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERCDCIC 107
                                                                          CVPSKVTKKYHEVLQLRP---KTGVRGLHKSLTDVALEHHEECDCVC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005576; C:extracellular; NAS.
GO; GO:0008083; F:growth factor activity, TAS.
GO; GO:0007417; P:central nervous system development; TAS.
                                                                                                                                                           Ź
                                                                                                                                                                                       Created)
                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AF091434, AAF00049.1; --
EMBL, AR033831; BAB03266.1; --
EMBL, AF260738; AAK51637.1; --
EMBL, AX358493; AAQ88857.1; --
                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000859; CUB
                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9JJSB; 1NTO
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
                                                        61
                                                                                                                                                                        Q9UL22;
                                                                                                                                                    09UL22
                                                                                                                             RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=White legiorn; TISSUE=Spinal cord;
MEDLINE=20317014; PubMed=10858496; DOI=10.1016/S0014-5793(00)01640-9;
Hamada T., Ui-Tei K., Miyata Y.;
"A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VEGF family.";
FEBS Lett. 475:97-103(2000).
-1- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
HSSP; Q9JJS8; INTO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                       'n
                                                                                                                                                                       50.5%; Score 318.5; DB 2; Length 345; 53.3%; Pred. No. 1e-26; sive 14; Mismatches 33; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 50.0%; Score 315.5; DB 2; Length 345; Best Local Similarity 52.8%; Pred. No. 2.2e-26; Matches 57; Conservative 16; Mismatches 30; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107
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                                                                                                                                                                                                                                                                                                                                                                                                            CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCIC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                296 CVPSKVTKKYHEVLQLRP---KTGVRGLHKSLTDVALEHHEECDCVC 339
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                                                                                                                   CDE9E51F40633E78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38940 MW; 97ACEA992BF5128C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Spinal cord-derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0016020; C:membrane; IEA.
GO; GO:0008083; F:growth factor activity; IEA.
GO; GO:0008283; P:cell proliferation; IEA.
GO; GO:0000074; P:regulation of cell cycle; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        345 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000859; CUB.
InterPro; IPR000072; PD_growth_factor.
Pfam; PF00441; CUB; 1.
ProDom; PD00142; PD_growth_factor.
ProDom; PD001629; PD_growth_factor; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
Pfam; PF00431; CUB; 1.
Pfam; PF00341; PDGF; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS560278; PDGF 2; 1.
SEQUENCE 345 AA; 39029 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF 2; 1.
                                                                                                                                                                                               Local Similarity 53.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00042; CUB; 1.
SMART; SM00141; PDGF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Growth factor; Mitogen SEQUENCE 345 AA; 38
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NCBI_TaxID=10090;
                         SEOUENCE
                                                                                           SEQUENCE
CKRARARARARAKKHHARARARARARKKILHARARKKAKKAKKKHHARAKKAKKAKKITAKKAKKKAKKAKKAKKAKKAKKAKKAKKAKKAKKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT 60
                                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAINWHUSTAT; TISSUE=Kidney;

MEDLINE=21092670; PubMed=11162582; DOI=10.1006/bbrc.2000.4187;

Hamada T., U1-Tei K., Imaki J., Miyata Y.;

Hamada T., U1-Tei K., Imaki J., Miyata Y.;

Rolenan Cloning of SCDGF-B, a novel growth factor homologous to scope/Pobfe-C/fallotein.";

Elochem. Biophys. Res. Commun. 280:733-737(2001).

C. '- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.

EMBL; AB033830; BAB19969.1; -.

SR HSSP; Q9JUSB; NITO.

GO: GO:0008083; F:ggrowth factor activity; IEA.

GO: GO:0008083; F:ggrowth factor activity; IEA.

GO: GO:0008083; F:ggrowth factor activity; IEA.

GO: GO:0008083; F:ggrowth factor.

RO; GO:00008083; F:ggrowth factor.

RO; GO:000074; P:regulation of cell cycle; IEA.

InterPro; IPRO00032; PD-growth_factor.

R Ffam; PF00341; CUB; 1.

R SMART; SM00042; CUB; 1.

R SMART; SM000441; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
25-GT-2004 (TrEMBLrel. 28, Last annotation update)
25-GT-2004 (TrEMBLrel. 28, Last annotation update)
26-UT-2004 (TrEMBLrel. 28, Last annotation update)
27-OT-2004 (TrEMBLrel. 28, Last annotation update)
28-GT-2004 (TrEMBLrel. 28, Last annotation adult male cecum cDNA, RIKEN full-length enriched library, clone:9130403008
27-OT-2004 (Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:4730022G11 product:platelet-derived growth factor, C polypeptide, full insert sequence) (Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:D93001MNB product:platelet-derived growth factor, C polypeptide, full insert sequence).
                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CVPRKYTKKYHEVLQLRP-KIGVKGLHK--SLTDVALEHHEECDCVC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCIC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38734 MW; F296DA6E9B765D10 CRC64;
                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.5%; Score 312.5; DB 2 54.2%; Pred. No. 4.8e-26; ive 15; Mismatches 31
                                      345 AA.
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                                                                 Created)
                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                               01-MAR-2001 (TrEMBLrel. 16, Create OL-MAR-2001 (TrEMBLrel. 16, Last e OL-CCT-2003 (TrEMBLrel. 25, Last e Spinal cord-derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE, PS01180, CUB, 1.
PROSITE, PS50278, PDGF_2, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 54.2
Matches 58; Conservative
                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                  Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Growth factor; Mitogen
SEQUENCE 345 AA; 38'
                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                      Name=rScdgf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296
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                                                   Q9EQX6;
                                     Q9EQX6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9QY71
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Q9QY71
          RESULT 9
Q9EQX6
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SECURATE ETCH TISSUE=Cecum, Cerebellum, and Head;

A Adachi J. Aizawa K., Akimura T., Azakawa T., Bono H., Carninci P.,

A Adachi J., Aizawa K., Akimura T., Azakawa T., Bono H., Carninci P.,

Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Kasukawa T.,

A Katoh H., Kawai J., Kojima Y., Kondo S., Konon H., Kouda M., Koya S.,

Katoh H., Kawai J., Kojima Y., Kondo S., Konon H., Kouda M., Koya S.,

A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

A Sasaki D., Sahibata K., Shinagawa A., Shizaki T., Sogabe Y., Tagami M.,

Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

Tomaru A., Toya T., Yasunishi A., Muramatus M., Hayashizaki Y.;

Submitted (Juli-2001) to the EmBil/GenBank/DDBJ databases.

-!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAINE-2049374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE-2049374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10.1617-1630 (2000).
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibate K., Itoh M., Aizawa K., Nagaoka S., Sasakin N., Carninci P., Konno H., Akiyama J., Nishi K., Ritsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamannoto H., Sakaguchi S., Inqegami T., Rashihwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Nkaraki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K., Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the RIKEN Genome Exploration Research Group Phase I & II Team;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K.,
Gilbertson D., West J., O'Hara P.J.,
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head; The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J;
                                                                           IISSUE=Ovary;
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Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                       345 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Pdgfc;
                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9JHV8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9JHV8
                                                                                                                                                                                                                                                                                                                                                                              Matches
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STRAIN-CZEGH II; TISSUB-Mammary tumor;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Duetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldow M.F., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., McWann P.J., McKernan K.J., Mark J.A., Gunazatne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Richards S., Worley K.C., Hale S., Garcia C., Shoretz A.M.,

Radan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rachiguez A.C., Gartimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Dones S.J., Marza M.A.;

T "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                MGD; MGI:1859631; Pdgfc.
GO; GO:0005515; C:extracellular space; TAS.
GO; GO:0005161; F:platelet-derived growth factor receptor bin. .; IDA.
GO; GO:0008284; F:pegulation efgular of cell proliferation; IDA.
GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. .; IDA.
GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; IDA.
                                                                                                                                                                                                                                                                                                                                                                            1 VDLDRINDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                   3,
                                                                                                                                                                                                                                                                                                                       Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCIC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                    296 CVPRKVTKKYHEVLQLRP---KTGVKGLHKSLTDVALEHHEECDCVC
                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                            38741 MW; 3A58A1F701B84EA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Platelet-derived growth factor, C polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                      49.4%; Score 311.5; DB 2; 52.3%; Pred. No. 6.2e-26; iive 15; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   345 AA
                                                                                                                                                                  InterPro; IPR000859; CUB.
InterPro; IPR000072; PD_growth_factor.
                                                                                                                                                                                         Pfan; PF00431; CUB; 1.
Pfan; PF00341; PDGF; 1.
SMART; SM00042; CUB; 1.
SMART; SM0141; PDGF; 1.
PROSITE; PS01180; CUB; 1.
Growth factor; Micogen.
SEQUENCE 345 AA; 38741 MW;
EMBL; AF117608; AAF22516.1;
EMBL; AF266467; AAK58566.1;
EMBL; AK033734; BAC28455.1;
                                        EMBL; AK042767; BAC31358.1;
EMBL; AK052947; BAC35216.1;
HSSP; Q9JJS8; 1NTO.
MGD; MGI:1859631; Pdgfc.
                                                                                                                                                                                                                                                                                                                                    Local Similarity 52.3% tes 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse con sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Pdgfc;
                                                                                                                                                                                                                                                                                                                       Query Match
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Matches
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Q8CI19
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organogenesis.";

Mech. Dev. 96:209-213(2000).

EMBL, AF286725; AAF91483.1; -.

RESP, Q9J368; 1NTO.

MGD; MG1:1859631; Pdgfc.

MGD; MG1:1859631; Pdgfc.

GO; GO:0005161; F:platelet-derived growth factor receptor bin. .; IDA.

GO; GO:0005161; F:platelet-derived growth factor receptor bin. .; IDA.

GO; GO:0005171; F:regulation of cell proliferation; IDA.

GO; GO:0007171; P:regulation of peptidyl-tyrosine phosphoryla .; IDA.

GO; GO:0007171; P:regulation of peptidyl-tyrosine kin. .; IDA.

InterPro; IPR000055; CD growth_factor.

InterPro; IPR000072; PD growth_factor.

SMART; SM00041; CUB; 1.

SMART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VDLDRLNDDAKRYSCTPRNYSVNI REELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
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MEDLINE=20417814; PubMed=10960785; DOI=10.1016/S0925-4773(00)00425-1;
Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
"The mouse Pddfc gene: dynamic expression in embryonic tissues during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.4%; Score 311.5; DB 2; Length 345; 52.3%; Pred. No. 6.2e-26; ive 15; Mismatches 33; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296 CVPRKVTKKYHEVLOLRP---KTGVKGLHKSLTDVALEHHEECDCVC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCIC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38741 MW; 9A58A05C6C0E9614 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-07T-2000 (TrEMBLrel. 15, Created)
01-07T-2000 (TrEMBLrel. 15, Last sequence update)
01-07T-2003 (TrEMBLrel. 25, Last annotation update)
Platelet derived growth factor C.
[2]
SEQUENCE FROM N.A.
STRAIN=CZECH II; TISSUE=Mammary tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF 2; 1.
Growth factor; Mitogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 52.3:
les 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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NCBI_TaxID=180454;
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NON TER
SEQUENCE
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0
                                                                                                                                                                           236 VNLNLLKEEVKLYSCTPRNFSVSIREELKRTDTRFWPGCLLVKRCGGNCACCLHNCNECO 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AgCP13204 (Fragment).
Name-agCG56469; ORFNames=ENSANGG0000014825;
Anopheles gambiae Str PEST.
Bukaryota; Metazoa; Atrhepoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                          3;
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0
                                                                Length 345;
                                                                                                                                                                                                                                                             CVPRKVTKKYHEVLQLRP---KTGVKGLHKSLTDVALEHHEECDCVC 339
                                                                                                                                                                                                                                    61 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCIC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.0%; Score 202; DB 2; Length 258; 57.4%; Pred. No. 5.5e-14; live 10; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP, Q9JGSS, INTO.

GO, GO:0016020; C:membrane; IEA.

GO, GO:000803; F:growth factor activity; IEA.

GO; GO:000811; P:cell growth and/or maintenance; IEA.

R InterPro; IPR000859; CUB.

R Pfam; PF00431; CUB; 1.

R PART; SM00042; CUB; 1.

R PROSITE; PS50279; PDGF_2; 1.
                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Sprague-Dawley; TISSUE=Skin;
Brown SA., Coberly D.M., Rohrich R.R., Chao J.J.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AFS00848; AAM47265.1; -
  PDGF 2; 1.
38886 MW; FA1486BED6D362F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29255 MW; 88625B989FCC3F8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Platelet-derived growth factor C (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last annotation update)
                                                                DB 2;
                                                           ch 48.4%; Score 305.5; DB 2; Similarity 52.3%; Pred. No. 2.8e-25; 56; Conservative 14; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                         258 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 26, Created) (TrEMBLrel. 26, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 57.4%
Marches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258
PROSITE; PS50278; P. SEQUENCE 345 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 AA;
                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
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01-MAR-2004
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NON TER
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COTOFMS
AC OTOFMS
DT 01-MP
DT 01-MP
DT 01-MP
DT NAME=
GN NAME=
GN NAME=
CO EAROPT
OC NEOPT
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 SCTPRNYSVNIR-EELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCTC--NSGKTVKKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.9%; Score 106.5; DB 2; Length 176; 28.9%; Pred. No. 0.0013; Live 17; Mismatches 39; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 AA; 20370 MW; F7630B2AFD67A59F CRC64;
                                                                                                                                                                    HSSP; P49763; IFZV.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0008083; F:growth factor activity; IEA.
GO; GO:0008283; P:cell proliferation; IEA.
GO; GO:000074; P:regulation of cell cycle; IEA.
InterPro; IPR004405; GF cySknot.
InterPro; IPR002400; GF cySknot.
Pfam; PF03128; CXCXC; 2.
Pfam; PF03128; CXCXC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 VTILEYRP---NKKDRFSHRELVPI--EEHVRCKCQC 100
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                                                                                                                                  preliminary data.
EMBL; AAAB01008846; EAA06182.1; -.
                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0438; GFCYSKNOT.
ProDom; PD001629; PD growth
PROSITE; PSS0278; PDGF 2; 1.
Growth factor; Mitogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 28.9%
Marches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   growth factor) (FIGF).
Name=Figf; Synonyms=Vegfd;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176
SEQUENCE FROM N.A.
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Mazitschek R., Krishnan J., Steffen A., Waltenberger J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 LNDDAKRYSCTPRNYSVNIREEL-KLANVVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_Taxip=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24; Gaps
linked by disulfide bonds before secretion. The fully processed VEGF-D is composed mostly of two VEGF homology domains (VHDs) bound by non-covalent interactions (By similarity). SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 (incomplete).
By similarity.
By similarity.
By similarity.
Interchain (By similarity).
Interchain (By similarity).
Interchain (By similarity).
N-linked (GLONAC. ..) (Potential).
N-linked (GLONAC. ..) (Potential).
N-linked (GLONAC. ..) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vascular endothelial growth factor D. Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 X 16 AA repeats of C-X(10)-C-X-C-X(1,3)-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00141; PDGF; 1.—Probom; PF00141; PDGF; 1.
Probom; PD001629; PD_growth_factor; 1.
SMART; SM00149; PDGF; 1; 1.
PROSITE; PS00249; PDGF 1; 1.
PROSITE; PS50278; PDGF 2; 1.
Angiogenesis; Cleavage on pair of basic residues; Glycoprotein; Growth factor; Mitogen; Multigene family; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KT---VKKYHEV---LQFEPGHIKRRGRAKTMALVDIQLDHHERCDCI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 ŞTSYISKQLFEISVPLTSVP------ELVPVKIANHTGCKCL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.5%; Score 104; DB 1; Length 326; 28.7%; Pred. No. 0.0046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (approximate).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF014827; AAB66557.1; -.
HSSP; P01127; 1PDG.
RGD; 620695; Figf.
InterPro; IPR000072; PD_growth_factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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MEDLINE=21541129, PubMed=11683876,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37112 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel, 19, 01-DEC-2001 (TrEMBLrel, 19, 01-JUN-2003 (TrEMBLrel, 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190
292
326 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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SEQUENCE
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CHAIN
PROPEP
DOMAIN
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Matches
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091ZE4
   SOUND BE SEED OF SOUND 
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REQUENCE FROM N.A.

SEQUENCE FROM N.A.

STAIN-Singapore local strain; TISSUE=Embryo;

RA STRAIN-Singapore local strain; TISSUE=Embryo;

RA Alteschal S.F., Featngold E.A., Grouse L.H., Derge J.G.,

RA Alteschal S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

RA Alteschal S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

RA Alteschal S.F., Jordan H., Moore T., Max S.L., Wang J., Haieh F.,

RA Distcherko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Usdin T.B., Toshivuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshivuki S., Carninci P., Prange C.,

RA Brownstein M.J., Weeken N.B., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan D.J., McKernan K.J., Malek J.A., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.,

RA T. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 IDBEWORTQCSPRETCVEVASELGKTTNTFFKPPCVNVFRCGGCC----NEESVMCMNT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 LNDDAKRYSCTPRNYSVNIREEL-KLANVVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSG
Pepper M.S., Giannis A., Sleeman J.P.;
"Characterization of indolinones which preferentially inhibit VEGF-C-
and VEGF-D-induced activation of VEGFR-3 rather than VEGFR-2.";
Eur. J. Biochem. 268:5530-5540(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBL TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
                                                                                                                                                                 -:- SIMILARITY: Balongs to the PDGF/VEGF growth factor family. BMBL; AY032728; AAK96008.1; -. HSSP; PO1127; IPDG. GO; GO: 001001620; C:membrane; IEA. GO; GO: 00108083; F:growth factor activity; IEA. GO; GO: 00008283; P:cell proliferation; IEA. GO; GO: 00008283; P:cell proliferation; IEA. Fam: PF00341; PDGF; 1. Progulation of cell cycle; IEA. Promp. PD001629; PDGF; 1. Promp. PD001629; PDGF; 1. PDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 KT---VKKYHEV---LQFEPGHIKRRGRAKTMALVDIQLDHHERCDCI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 STSYISKQLFEISVPLTSVP------ELVPVKIANHTGCKCL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.5%; Score 104; DB 2; Length 326; 28.7%; Pred. No. 0.0046; ive 16; Mismatches 37; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37106 MW; D7CAEBA6C9FABB7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Singapore local strain; TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00141; PDGF; 1.
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 28.79
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Growth factor; Mitogen
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9
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Lung;

MEDLINE=98140120; PubMed=9479493; DOI=10.1006/geno.1997.5079;

MEDLINE=98140120; PubMed=9479493; DOI=10.1006/geno.1997.5079;

Roschigiani M., Lestingi M., Luddi A., Orlandini M., Franco B.,

Rossi E., Ballabio A., Zuffardi O., Oliviero S.;

"Human FIGF: Cloning, gene structure, and mapping to chromosome Xp22.1

Detween the PIGA and the GRPR genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 ANVVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=9818549; bubMed=9435229; DOI=10.1073/pnas.95.2.548; MEDLINE=98188549; bubMed=9435229; DOI=10.1073/pnas.95.2.548; Achen M.G. Jeltsch M., Kukk E., Maekinen T., Vitali A., Wilks A.F., Alitalo K., Stacker S.A.; Furence T., Vitali A., Wilks A.F., Alitalo K., Stacker S.A.; Forctor I (VEGF) is a ligand for the tyrosine kinases VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flt4)."; Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97349118; PubMed=9205122; DOI=10.1006/geno.1997.4774;
Yamada Y., Nezu J.-I., Shimane M., Hirata Y.;
"Molecular cloning of a novel vascular endothelial growth factor,
            16.2%; Score 102; DB 2; Length 194; 33.8%; Pred. No. 0.0044;
                                                                                                                                                                                                                                                                                                                                                                                                                24; Indels
                                                                                                                                                                                                                                                              PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
Growth factor; Hypothetical protein; Mitogen.
SEQUENCE 194 AA; 22651 MW; 583C3B9972B09795 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 ALVDIQLDHHERCDCICSSR 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 -- VQVQLEDH--LECVCTSR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        growth factor) (FIGF).
Name=FIGF; Synonyms=VEGFD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics 42:483-488(1997).
                                                                                                                                                                                                                                                                                                                                                                     Query Match 16.2%
Best Local Similarity 33.8%
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 CKPRDTVVYLGEEYPESTNLQYNPRCVTVKRCSGCCNGDGQICTAVETRNTTVTVSVTGV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 -----CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCI-----CS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (Rel. 44, Last annotation update)
Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 CTPRNYSVNIREEL-KLANVVFFPRCLLVQRCGGNCG----CGTVNWRSCT---
                                                                                                                                                                                                                                                                                                                                   Vascular endothelial growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.9%; Score 100.5; DB 1; Length 148; 25.6%; Pred. No. 0.0048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Interchain (By similarity)
Interchain (By similarity)
N-linked (GlcNAc. .) (Po
                                                                                                                                                                                                                                                                                                                                                                                                                                                         16078 MW; FOEI3BAI04CC73F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 93:11675-11680(1996)
                                                                                                                                                                                                                                                                                              Glycoprotein; Growth factor; Mitogen; Signal. SIGNAL 1 25
                                                                                                                                                                                                                                                                                                                                                                  By similarity.
By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
                                                                                                                                                                InterPris; IPR002400; GF_Cysknot.
InterPro; IPR002400; BD_Growth_factor.
Pfam, PF00341; PDGF; 1.
PRINTS; PR00438; GFCYSKNOT.
ProDom; PD001629; PD_Growth_factor; 1.
SMMRT; SN00141; PDGF; 1.
PROSITE; PS00249; PDGF 1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                      Potential.
                                                                                                                                                                                                                                                                                                                                                    homolog
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28-FEB-2003 (Rel. 41, Last seq
                                                                                                                       EMBL; S67522; AAB29223.1; -. PIR; D49530; D49530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  growth factor) (FIGF).
Name=Figf; Synonyms=Vegfd;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                       HSSP; P15692; 2VPF
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R GO; GO:0005615; C:extracellular space; TAS.

R GO; GO:0005101; F:platelet-derived growth factor receptor bin. .; TAS.

R GO; GO:0005102; F:receptor binding; TAS.

R GO; GO:000284; P:positive regulation of cell proliferation; TAS.

R InterPro; IPRO00072; PD growth_factor.

R InterPro; IPRO00072; PD growth_factor.

R ProDom; PRO01529; DD growth_factor.

R PROSITE; PSO0249; PD growth_factor; 1.

R MART: SM00141; PDGF; 1.

R PROSITE; PSS0278; PDGF; 1.

R PROSITE; PSS0278; PDGF; 1.

R PROSITE; PSS0278; PDGF 2: 1.

R PROSITE; PSS0278; PDGF 2: 1.

R Majlogenesis; Cleavage on pair of basic residues;

W Multigene family; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 LNDDAKRYSCTPRNYSVNIREEL-KLANVVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ort virus (strain NZ7) (OV NZ-7).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Parapoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lyttle D.J., Fraser K.M., Fleming S.B., Mercer A.A., Robinson A.J., "Homologs of vascular endothelial growth factor are encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                             By similarity.
By similarity.
By similarity.
Interchain (By similarity).
Interchain (By similarity).
N-linked (GlOWAC. . .) (Potential).
                                                                                                                                                                                                                                                                                    Vascular endothelial growth factor D.
                                                                                                                                                                                                                                                                                4 X 16 AA repeats of C-X(10)-C-X-C-X(1,3)-C.
1 (approvies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Virol. 68:84-92(1994).
-!- FUNCTION: Induces endothelial proliferation.
-!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
-!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 STSYISKQLFEISVPLTSVP-----ELVPVKVANHTGCKCL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 KT---VKKYHEV---LQFEPGHIKRRGRAKTMALVDIQLDHHERCDCI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.2%; Score 102; DB 1; Length 354; 28.7%; Pred. No. 0.0083; cive 16; Mismatches 37; Indels ;
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01-0CT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Vascular endothelial growth factor homolog precursor.
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Orf virus (strain NZ7)
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nes 31; Conserv
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MEDLINE-97349118; PubMeds 9205122; DOI-10.1006/geno.1997.4774;

"Media da. Natu J. T. Shikane M. Haraa Nijaraa Nijaraa
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107 IDEEWQRTQCSPRETCVEVASELGKTTVTFFKPPCVNVFRCGGCC----NEEGVMCMNT 161
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ches 38; Indels
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ive 16; Mismatches
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              GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polypeptides comprising an epitope-bearing portion human or murine ZVEGF3 (vascular endothelial growth factor homologue) are claimed. The growth factor domain and a CUB domain (generic sequence comprises a growth factor domain and a CUB domain (generic sequence motifis are shown in AAY9686). The growth factor domain is characterized by an arrangement of cysteine residues and betastrands that is characteristic of the "cysteine knot" structure of the platelet-derived growth factor (PDGF) family. The CUB domain shows homology to CUB domains in neuropilins, human bone morphogenetic protein.

I, porcine seminal plasma protein, bovine acidic seminal fluid protein and Xenopus leavis tolloid-lins, bundan bone morphogenetic protein.

Compared that ZVEGF3 polypeptides complex with a second polypeptide to predict that ZVEGF3 polypeptides complex with a second polypeptide to circmosome 4q28.3 ZVEGF3 is useful for stimulating the growth of fibroblasts or smooth muscles cells, for activating cell surface PDGF-alpha receptor and for inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is useful for regulating (post-development) organ growth, regeneration and maintenance, as well as tissue maintenance and crepair processes. ZVEGF3 antagonists are useful for treating cancer, rheumatoid arthritis, diabetic retinopathy, ischemic limb disease, crepair processes. ZVEGF3 antagonists are useful for treating center growth chemmatoid arthritis, wound healing, chronic liver disease and heperplasia, atherosclerosis, wound healing, chronic liver disease and chemmangiona formation. ZVEGF3 can also be used to modulate neurite growth and development of the nervous system, and for treating neurodegenerative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fibroblasts comprising an
 Adb26079 Human
Adb21564 Novel
                                                                                                                                                                                                                             Vascular endothelial growth factor; homologue; zvegf3; CUB domain; Cysteine knot; platelet-derived growth factor; pDGF; neuropilin; chronosome 4q28.3; cytostatic; anti-psoriatic; anti-inflammatory; anti-diabetic; ophthalmological; anti-theumatic; anti-arthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel zvegf3 polypeptides and nucleotides encoding them useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shoemaker KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epitope bearing portion of a specific amino acid sequence.
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                                                      ALIGNMENTS
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 ADB26079
ADB21564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stimulating growth of smooth muscle
                                                                                                                       AAY96864 standard; protein; 370 AA
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                                                                                                                                   1 MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDESNHLTDLYRRDETIQVKG
                                                                                                                                                                                                                       61 NGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRYDFVEVEDIS
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                                                                                                                                                                                             NGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRYDFVEVEDIS
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  Length 370;
                                                Indels
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100.0%; Score 1994; DB 3; 100.0%; Pred. No. 1e-188;
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                                             Mismatches
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10-NOV-1999; 99US-0164463P.
04-FEB-2000; 2000US-0180169P.
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                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DCICSSRPPR
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N-PSDB; AAC81555.
                         Similarity
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(first entry)

08-SEP-2000

AAY71130;

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The invention relates to the human growth factor homologue zvegf4

(AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member of the PDGF (platelet-derived growth factor)/VGGF (vascular endothelial growth factor) family. Zvegf4 has a growth factor domain (AAB4864)

C growth factor) family. Zvegf4 has a growth factor domain (AAB4864)

C characterised by a PDGF cystine knot structure, and a CUB domain (AAB48655) which has a beta barrel structure, and a CUB domain (AAB48655) which has a beta barrel structure, vacef4 has PDGF-like activity, having mitogenic activity on fibroblasts, vascular smooth muscle cells and pericytes, and has also been shown to stimulate bone of growth. The invention also relates to fusion proceins comprising human zvegf4 nucleic acids, the recombinant expression of human zvegf4 numan zvegf4 or fragments thereof, particularly human zvegf4 numan zvegf4 acids, the recombinant expression of human zvegf4 an antibody which binds to human zvegf4 or a fragment thereof; a method of activating a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a method of method of detecting a genetic abnormality in the coll between the proliferation, differentiation, migration or metabolism of polypeptides; and a method of detecting a genetic abnormality in the crowfile and polypeptides and a method of detecting a genetic abnormality in the crowfile and polypeptides and a method of detecting a genetic abnormality in the crowfile and method of detecting a genetic abnormality in the crowfile and method of detecting and derived fragments may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used to stimulate tissue development or repair, or cellular treatment or repair of treatment or repair of liver damage, and may also be used to modulate neurite growth (e.g., in the treatment of Alzheimer's disease or multiple sclerosis). Due to their osteogenic activity, they may be used in the treatment of periodontal disease and fractures. They may also be used to enhance expansion and mobilisation of haematopoietic stem cells and endothelial precursor stem cells, which may be useful in the treatment of ischaemia, in wound healing, and in the modulation of the immune system.
   factor homologs and the nucleic acids that encode them, useful
                                   treating liver damage, ischemia, multiple sclerosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents human zvegf4
                                                                                                                                        Claim 1; Page 110-111; 143pp; English.
                                       e.g. for treating li
Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 370 AA;
Growth
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1 MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDESNHLTDLYRRDETIQVKG Gaps . 0 Length 370; Indels DB 3; .. Score 1994; DB 3; Pred. No. 1e-188; 0; Mismatches 0 Query Match
Best Local Similarity 100.0%;
Matches 370; Conservative 0 엄

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RCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTWALVDIQLDHHERC 360 301

DCICSSRPPR 370 DCICSSRPPR 361

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Score 1994; DB 3 Pred. No. 1e-188; ; Mismatches 0

100.0%; Sc 100.0%; Px :ive 0;

Best Local Similarity 100. Matches 370; Conservative

Similarity

Query Match

Sequence 370 AA;

Length 370;

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1 MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDESNHLTDLYRRDETIQVKG

DD DD ð

AAY71130 standard, protein, 370 AA. RESULT 3
AAY71130
ID AAY7.

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The present sequence is the complete human platelet derived growth factor (PDGF)-D, formally known as Vascular Endothelial Growth Factor (VEGF)-G. It is derived from human feetal lung lambdagilo CDNA library. It belongs to the VEGF/PDGF family. It functions as an activator of proliferation, differentiation, growth and motility of cells, that express PDGF-D receptor. This sequence is useful for inhibiting the growth of tumours, that express PDGF-D. Expression of PDGF-D and its proteolytic cleavage for generating an activated truncated form is useful for regulating receptor binding specificity of PDGF-D. PDGF-D antagonist is useful for inhibitining tissue remodelling during the invasion of tumour cells into mormal cells. PDGF-D may be used to treat wounds, atherosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a platelet-derived growth factor, useful for diagnostic and therapeutic applications, e.g. concerning cancer.
                                                                                                                                                                                                                                       /label= CUB_domain
/note= "Participates in protein-protein or carbohydrate
                                                                                               Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnerary;
                                                                                                           VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tun
proliferative; activator; proliferation; differentiation; motility;
growth; PDGF-D receptor; antagonist; tissue remodelling; treat;
atherosclerosis; wound; metastasis.
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                                                                  Human Platelet Derived Growth Factor (PDGF)-D protein.
                                                                                                                                                                                                                                                                                  254. .257
/label= Proteolytic site
/note= "Dibasic motif"
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98US-0113997P.
99US-0150604P.
99US-0157108P.
                                                                                                                                                                                                                                                                     interactions"
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04-OCT-1999;
05-OCT-1999;
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07-SEP-2001 (first entry)
                                                                                      Matches 370; Conservative
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                                                                 Similarity
Sequence 370 AA;
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04-JAN-2000;
03-MAR-2000;
10-MAR-2000;
08-AUG-2000;
12-SEP-2000;
20-SEP-2000;
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                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and treatment of deregulared cell growth e.g. cancer, disorders involving aberrant angiogenesis e.g. psoriasis, and chronic inflammatory diseases.
                                                                                                                                                                                                                                                                                                         LDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIRBELKLANVVFFPRCLLVQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vascular endothelial growth factor family member used for diagnosis
                          NGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEBAENDICRYDFVEVEDIS
                                                                                                                      TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMY
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NGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRYDFVEVEDIS
                                                                                         ETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLEDFQPAAASE
                                                                                                                                                                                  TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vascular endothelial growth factor; VEGF; cancer; cell; angiogenesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DCICSSRPPR 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human VEGF-G protein.
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                                                                          Gaps
                                                                       0
                 Length 370;
                                                                       Indels
Score 1994; DB 4;
Pred. No. 1e-188;
Orienhes 0;
                                                                       0; Mismatches
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990S-0159231P.
2000US-0174485P.
2000US-0186707P.
2000US-0188250P.
                 100.0%;
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2000US-0234082P.
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Human FCTR1 protein present in clone 30664188.0.99

07-SEP-2001 (first entry)

AAU00698;

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The sequence represents a protein related to bone morphogenetic protein-1 (BMP-1), vascular endothelial growth factor (WEG-E) and platelet derived growth factor (PDGF). Polypeptides and polynucleotides related to BMP-1, VEGF-E and PDGF are referred to as FCHRX peptides and nucleic acids.

C WEGF-E and PDGF are referred to as FCHRX peptides and nucleic acids.

FCTRX proteins are useful for treating or preventing a disorder.

C FCTRX proteins are useful for treating or preventing a disorder.

C FCTRX proteins are useful for the proteins in a mammal, where the alsorder is characterised by insufficient or ineffective growth of a cell or a tissue, e.g. hyperplasia or neoplasia. The peptides and their associated nucleic acids are useful for both promoting and inhibiting growth of cells and tissues and in treatment of cancer, anaemia, casociated nucleic acids are useful for both promoting and inhibiting growth of cells and tissues and in treatment of cancer, anaemia, albaldness, for treating cardiovascular and fibroric disorders, inflammatory disorders, neurodegenerative disorders, osteoarthritis, inflammatory disorders, neurodegenerative disorders such as haemophilia, and neural disorders including Parkinson's disease, allaheimer's disease, multiple solerosis, Huntington's disease, anyotrophic lateral sclerosis, peripheral neuropathy, acute brain injury
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                                                                                                                                                            useful for
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                                                                                                                                               treating cancer, cardiovascular and fibrotic diseases, diabetic ulcers, wound healing and neuronal disorders.
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                                         Minskoff S;
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                                         Boldog FL,
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                                     Herrmann JL,
                                                                                                                                                                                                                                       Disclosure, Fig 13, 171pp, English
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100.0%;
                                         Lichenstein H,
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Best Local Similarity 100.
Matches 370; Congervative
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(CURA-) CURAGEN CORP.
                                                                                                  2001-316172/33.
                                                                                               WPI; 2001-316172,
N-PSDB; AASO4498
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                                     Shimkets RA,
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AAU00698 gtandard; protein; 370 AA.

RESULT 6 AAU00698

DCICSSRPPR 370

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The sequence represents a protein related to bone morphogenetic protein-1 (BMP-1), vascular endothelial growth factor (VEGF-E) and platelet derived growth factor (PDGF). Polygeptides and polymocleotides related to BMP-1, VEGF-E and PDGF are referred to as FCTRX peptides and muclic acids. FCTRX proteins are useful for treating or preventing a disorder associated with aberrant expression, aberrant processing, or aberrant physiological interactions of the proteins in a mammal, where the disorder is characterised by insufficient or ineffective growth of a cell or a tissue, e.g. hyperplasia or neoplasia. The peptides and their associated nucleic acids are useful for both promoting and inhibiting
                                                                                                                                                                         Bone morphogenetic protein-1; BMP-1; vascular endothelial growth factor; VEGF-E; platelet derived growth factor; PDGF; FCTRX; hyperplasia; cancer; neoplasia; anaemia; leukopenia; baldness; cardiovascular disorder; fibrotic disorder; diabetic uler; obesity; hyperproliferation; human; dysproliferation; neurodegenerative disorder; osteoarthritis; epilepsy; inflammatory disorder; Graft versus host disease; coaqulation; haemophilia; neural disorder; Parkinson's disease; Alzheimer's disease; multiple sclerosis; Huntingfon's disease; amyotrophic lateral sclerosis; peripheral neuropathy; acute brain injury.
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/note= "Metallothionein domain"
350. .362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    location/Qualifiers
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04-JAN-2000; 2000US-0174485P.
03-MAR-2000; 2000US-0186707P.
10-MAR-2000; 2000US-0188250P.
08-AUG-2000; 2000US-0223879P.
12-SEP-2000; 2000US-00662783.
20-SEP-2000; 2000US-0234082P.
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/note= "Mages 
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N-PSDB; AAS04492.
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WO200157083-A1.
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growth of cells and tissues and in treatment of cancer, anaemia, leukopenia, baldiness, for treating cardiovascular and fibrotic disorders, diabetic ulcers, obesity, infectious diseases, hyperproliferative and dysparoliferative disorders, neurodegenerative disorders, osteoarthritis, inflammatory disorders, Graft versus host disease, coaquiation disorders such as haemophilia, and neural disorders including Parkinson's disease, Alzheimer's disease, multiple sclerosis, Huntington's disease, amyotrophic lateral sclerosis, peripheral neuropathy, acute brain injury
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                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bone cancer; osteonecrosis; bone defect; osteogenesis; osteoporosis; osteoporosis;
                                                                                                                                                 ..
                                                                                                                             DB 4; Length 370;
                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e≂ "propeptide-like sequence"
.370
                                                                                                                            ; Score 1994; DB 4
; Pred. No. 1e-188;
0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "mature protein"
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100.0%;
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                                                                                                                                                 Matches 370; Conservative
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                                                                                                                                       Similarity
                                                                                                        Sequence 370 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human zvegf4
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                                                                                     epilepsy
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The invention relates to the use of zvegf4 polypeptide for promoting bone, ligament or cartilage growth in a mammal, and for promoting bone, ligament or cartilage growth in a mammal, and for promoting cartilage or bone marrow stem cells in culture. For promoting cartilage growth, chondrocytes are cultured ex vivo in presence of the zvegf4 polypeptide and then placed into mammal where cartilage is to be grown. Zvegf4 polypeptide is useful for promoting growth of bone, ligament or cartilage in a mammal at a site of bony defect such as fracture, bone graft, implant or periodontal pocket, in humans and non-human animals such as domestic animals including livestock and companion animals. Zvegf4 is used for promoting growth of bone, ligament, or cartilage in conditions of bone defects following therapeutic treatments or decreased bone formation, or elevation of peak bone mass in premenpausal woman. It is also useful for healing bone following radiation induced osteonecrosis, repairing bone defects arising from surgery, and curing distraction osteogenesis, treating bone injuries including repair of cartilage and ligament and treatment of osteoporosis. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
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                                                                                                                                                                                                                                                                                                                                                                                                                         Use of zvegf4 polypeptide for promoting bone, ligament or cartilage growth in mammal at site of fracture, implant, and bone graft, and promoting growth or differentiation of osteoblasts, chondrocytes in culture.
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100.0%; Pred. No. 1e-188;
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31-MAR-2000; 2000US-00540224.
                                                                                                                                                                                                            (ZYMO ) ZYMOGENETICS INC.
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                                                                                                                                                                                                                                                                                                                                   WPI; 2001-611088/70.
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                                                                                                                                                                                                                                                                      Gilbertson DG,
                                                      03-MAY-2000;
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09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Secreted protein, immunosuppressive, antiarthritic; antirheumatic; antiproliferative, cytostatic; cardiant, vasotropic; cerebroprotective, nootropic; neuroprotective; antibacterial; virucide; fungicide; human;
                                                                                                                                                                                                                                                                                                                                                                    121 ETSTIIRGRWCGHKEVPPRIKSRINQIKIIFKSDDYFVAKPGFKIYYSLLEDFQPAAASE
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                                                                                                                                               1 MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDESNHLTDLYRRDETIQVKG
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                                                                                              Gaps
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Choi GH;
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                                              Length 370;
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Shi Y,
                                                                                            Indels
                                              DB 4;
                                           100.0%; Score 1994; DB 4;
100.0%; Pred. No. 1e-188;
ive 0; Mismatches 0;
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P, Ebner R, Duan DR,
SM, Barash SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein (clone Id HGCNC48).
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Moore PA, Wei P,
Ni J, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           opthalmalogical; gene therapy
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04-FEB-2000; 2000US-0180628P.
12-SEP-2000; 2000US-0231968P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                       Best Local Similarity 100.
Matches 370; Conservative
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Sequence 370 AA;
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Olsen HS, Mo
Fiscella M,
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proliferation or extracellular matrix production, treating fibrosis and
reducing stellate cell activation in a mammal. The method comprises
administering a composition containing a 2vegf3 antagonist in combination
with a delivery vehicle. The Zvegf3 as a protein that is structurally
related to platelet-derived growth factor (PDGP) and the vascular
endothelial growth factors (VGCP). The Zvegf3 protein is also designated
as "VEGF-R" and "PDGF-C". The Zvegf3 antagonist is useful to block the
mitogenic effects of zvegf3 and thereby to inhibit or prevent and treat
ce mitogenic effects of zvegf3 and thereby to inhibit or prevent and treat
ce habelis, sclerodderma, fibrotic disorders of liver such as chronic active
thepatitis, tulminant viral hepatitis, post necrotic cirrhosis and alpha-1
centitrypsin deficiency, fibrotic disorders of the kidney such as
chronical disorders of the viral arteriosclerosis, fibrotic disorders
contential such as silicosis, absetosis, idiopathic pulmonary hypertension,
fibrotic disorders of panoreas, fibroproliferative disorders of the
chasculature guch as transplant vasculopathy and fibroproliferative
disorders of the bone such as osteoperrosis and hyperostosis. The present
                                                                                                                                                                                                                                                                                                                                                            Human; Zvegf3 antagonist, cell proliferation; stellate cell activation; extracellular matrix production; fibrosis; VEGF-R; PDGF-C; platelet-derived growth factor; PDGF; vascular endothelial growth factor; PGGF; mitogenic effect; therapy; keloid; scleroderma; fibrotic disorder; chronic active hepatitis; fulminant viral hepatitis; amyloidosis; abbestcosis; renal arteriosclerosis; post necrotic cirrhosis; asbestcosis; renal arteriosclerosis; focal glomerulosclerosis; focal glomerulosclerosis; pulmonary fibrosis; osteopetrosis; pulmonary fibrosis; osteopetrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bronchiolitis obliterans-organising pneumonia; transplant vasculopathy; fibroproliferative disorder; Zvegf4 protein.
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                                                                                                                                                                                                                                                                                                                   Human gvegf4 protein which forms heteromultimer with Zvegf3 protein.
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                                                                                                                                                                      AAE00999 standard; protein; 370
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12-NOV-1999; 99US-0165255P.
01-AUG-2000; 2000US-022223P.
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                                      361 DCICSSRPPR 370
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DCICSSRPPR
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used to prevent, treat or ameliocate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can also be used in diagnosting a pathological condition. The antibodises to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, viruses and fungi and ardioimans disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, common chemotaxis. The polypeptides can also be used as a food additive or present preservative to increase storage capabilities. The present
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                                                                         The invention provides novel human secreted proteins and polynucleotides encoding them. The secreted proteins can be expressed by standard recombinant methodology. The secreted proteins and polynucleotides are
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to preventing, treating or ameliorating a medical condition.
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100.0%; Pred. No. 1e-188;
iive 0; Mismatches 0
                                    Claim 11; Page 447-449; 482pp; English
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Best Local Similarity
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The present invention relates to LPBS, an analogue of platelet-derived growth factor (PDGF) homologue. Sequences of the invention are useful for the manufacture of a medicament for treating musculoskeletal disorder (MSD) which include promoting bone growth, cartilage differentiation and function, wound healing, neuron growth, preventing cartilage degradation osteoporosis, osteopenia, arthritis, sarcopenia, por factures, tissue atrophy, traumatised connective tissues and/or transplanted organs, bone or muscle loss due to malignancy, endocrine disorders and immobility. They are also used for prophylactically increasing or maintaining bone density in a mammal. The present sequence is human LPBS protein
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therapy; bone growth; cartilage differentiation; wound healing;
            neuron growth; bone fracture; osteoporosis; osteopenia; arthritis; sarcopenia; periodontal disease; tissue atrophy; endocrine disorder; muscle loss; immobility; bone density.
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/label= Signal_peptide
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11-JAN-2001; 2001US-0261071P.
11-JAN-2001; 2001US-0261076P.
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hes 370;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prayaga S, Boldog FL, Yang M, Burgess CE;
Shimkets JB, Larochelle WJ, Lichenstein HS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating, delaying the onset of, or ameliorating an inflammatory pathology (e.g. inflammatory bowel disease or Crohn's disease) by administering to the subject fibroblast growth factors or a combination of growth factors.
                                                                                                                                                                                                                          FCTR1; platelet derived growth factor D; PDGFD; human; Crohn's disease; inflammatory bowel disease; gene therapy; antiinflammatory; vulnerary;
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/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                24. 370
/label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                               /note= "PDGF domain"
302. .365
/note= "metallothione
350. .362
/note= "PDGF domain"
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                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              "CUB domain"
                                                                                                                                               ABB79643 standard; protein; 370 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2000; 2000US-0246206P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-NOV-2001; 2001WO-US043846
                                                                                                                                                                                                                                              cytostatic, cardiovascular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rittman B,
                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                       .306
                                                                                                                                                                                                                                                                                                                                   .167
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                                                                                             DCICSSRPPR 370
                                                                           DCICSSRPPR 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-599742/64.
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                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                 ABB79643;
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                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                 Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
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deletion variants, and methods of using these to treat, delay the onset of, or ameliorate, an inflammatory pathology, especially inflammatory bowel disease, a disease that occurs in the colon or small intestine, or Crohn's disease (all claimed). FGFCX and FCTRX polypeptides and deletion variants are also useful for treating growth and proliferative diseases such as cancer, angiogenesis, collagen formation, fibrotic and cardiovascular diseases or diabetic ulcers, and in wound healing. They can be used in screening and detection methods, chromosome mapping, tissue typing, predictive medicine, diagnostic assays, prognostic assays, and pharmacogenomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDESNHLTDLYRRDETIQVKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1994; DB 5;
100.0%; Pred. No. 1e-188;
ive 0; Mismarches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 370; Conservative
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us-10-606-055-2

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TINWESVISSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMY
                                                                                                                                                                                                                                                                                            AAB47891 standard; protein; 370 AA.
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99US-0142576P.
99US-0161653P.
99US-0165255P.
99US-00457066.
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                                                                                                                                                                                           DCICSSRPPR 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-171026/22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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06-JUL-1999;
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12-NOV-1999;
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AAB47891
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                                                                                                                                                                                                                                                                                             The invention relates to an isolated polypeptide, designated zvegf3 (a vascular endothelial growth factor-like protein) of 111-136 amino acid residues in length and comprises the sequence appearing as AB632889 from residues in length and comprises the sequence appearing as AB632889 from residues in length and second polypeptide an isolated protein (c comprising a first polypeptide disulphide bonded to a second polypeptide, where each of the first and second polypeptides is from zvegf 3, and comprising an example of the protein medulates cell poliferation, differentiation, metabolism or migration, the zvegf 3 encoding polymoleotides and zvegf 3 expression vectors and host cells. Zvegf 3 is useful as additives in c fissue adhesives for promoting revascularisation of the healing tissue, for designing molecules that antagonise semaphorin-stimulated activities, including neurite growth, cardiovascular development, cartilage and limb development, and T and B-cell function, and for imaging tumours or other sites of abnormal cell profileration and in gene therapy applications. The proteins are useful therapeutically to stimulate tissue development or repair, or cellular differentiation or proliferation, for stimulating the growth of fibroblast or smooth muscle cells, as molecular weight correction or as standards in the analysis of cells, as uncommune growth of solid tumours, for treating diabetic retinopathy, glomerulosand atthritis, various forms of cencers, autoimmune cellbrosis, including scar formation, keloids, liver fibrosis, lung fibrosis, skin grafting, and female reproductive tract disorders, chronic liver disorders of chromation, wordsordal isohaemia, solaropathy), glomerulosclerosis, atherosclerosis, skin wounds, chospease, disease, dirculatory disorders of, heart failure, hepatic or portal vein thrombosis, cardiac sclerosis, neurodegenerating neurite outgrowths following strokes. The greener and for regenerating neurite outgrowths following strokes. The greener represents
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                                                                                                                                                                                                               Novel polypeptide, designated zvegf3 useful for treating skin wounds, ulcers, burns, skin grafting, female reproductive tract disorders,
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                                                                                                                                Shoemaker KE;
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                                                                                                                                Sheppard PO,
                                                                                                                                                                                                                                 ulcers, burns, skin grafting, female reproduct
Parkinson's disease, and Alzhelmer's disease.
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                                                                                                                                                                                                                                                                           Disclosure; Col 95-98; 68pp; English.
                                                                                                                               Piddington CS,
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                         98US-0111173P.
99US-0142576P.
99US-0161653P.
99US-0165255P.
99US-00457066
                                                                                                  ZYMO ) ZYMOGENETICS INC
                                                                                                                                           West JW;
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                                                                                                                                                                                          N-PSDB; ABS68643.
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                                                                                                                                            Gilbertson DG,
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07-DEC-1999;
                           07-DEC-1998;
                                                      21-OCT-1999
                                                                       12-NOV-1999;
                                          06-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; mouse; zvegf3; zvegf4; platelet derived growth factor; PDGF; homolog; growth; bone. Ligament; cartilage; profileration; osteoblast; chondrocyte; bony defect; fracture; bone graft; implant; periodontal pocket; osteoclast; bone marrow stem cell; osteoporosis.
TWWESVISSISGVSYNSPSVIDPILIADALDKKIAEFDIVEDLLKYFNPESWQEDLENMY
                                                                                                                                                                                                       RCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC
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30-OCT-2000; 2000US-0244479P
                             (ZYMO ) ZYMOGENETICS INC.
                                                                      WPI; 2002-590847/63.
N-PSDB; ABN84420.
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                                                                                                                                                                                     ETSTIIRGRWCGHKEVPPRIKSRTWQIKITFKSDDYFVAKPGFKIYYSLLEDFQPAAASE 180
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                                                                                                                                                                                                                                                                                                               RCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTWALVDIQLDHHERC 360
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/label= Growth_factor_domain+Interdomain
246. .370
/label= Growth_factor_domain
/note= "alternatively comprises residues 250-370 or 258-370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-370,
                                                                                                                                                                                                                                                                       LDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQ
                                                                                                    1 MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDESNHLTDLYRRDETIQVKG
                                                                                                                   1 MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDESNHLTDLYRRDETIQVKG
                                                                                                                                                                                                                                                   TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWOEDLENMY
                                                                                                                                                                                                                               TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMY
                                                                                  Gaps
osteoclasts, chondrocytes or bone marrow stem cells, where the bone marrow stem cells are harvested from a patient prior to culture. The method is therefore useful for treating osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19. 370 — 19. Jahola domain+growth factor domain /Jahola CUB domain+interdomain+growth factor domain Jhoce = "alternatively comprises residues 24-370, 25-370 or 52-370"
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0
                                                             Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zvegf4; human; kidney; acute tubular necrosis; nephrotropic;
gene therapy.
                                                           Query Match
100.0%; Score 1994; DB 5;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 370; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .18
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               ABB79588 standard; protein; 370 AA.
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                                                                                                                                                                                                                                                                                                                                                         DCICSSRPPR 370
                                                                                                                                                                                                                                                                                                                                                                             DCICSSRPPR 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human zvegf4 protein.
                                         Sequence 370 AA;
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                                                             Query Match
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 LDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
Improving kidney function, or enhancing proliferation or survival of kidney tubule epithelial cells or epithelial cell precursors in a mammal comprises administering a zvegf4 protein or zvegf4 protein-encoding polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDESNHLTDLYRRDETIQVKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDESNHLTDLYRRDETIQVKG
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100.0%; Pred. No. 1e-188;
ive 0; Mismatches 0;
                                                                                      Claim 4; Page 38-39; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 370; Conservative
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Best Local Similarity
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us-10-606-055-2

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                                                                                                       RCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
                                                                                                                       RCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTWALVDIQLDHHERC 360
                                                                                                                                                                                                                                                                                                                                                                                            Human; secreted protein; autoimmune disease; blood coagulation disorder; blood platelet disorder; hyperproliferative disorder; renal disorder; neurodegenerative disorder; cardiovascular disorder; respiratory disorder; endocrine disorder; reproductive disorder; proteintestinal disorder; infectious disease; antianamanic, cytostatic; antiarthritic; immunosuppressive; antiasthmatic; antidiabetic; antiparkinsonian; neuroprotective.
TWWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMY
                                                             LDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQ
                                            LDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREBLKLANVVFFPRCLLVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New secreted polypeptides and encoding polynucleotides, useful for preventing, treating and diagnosing diseases e.g. anemia, cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DR;
Choi GH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CE,
DR,
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Duan
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Barash SC;
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                                                                                                                                                                                                                                                                        AA.
                                                                                                                                                                                                                                                                        ABG76575 standard; protein; 370
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2000US-0180628P.
2000US-0231968P.
2001WO-US001431.
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Ni J, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001US-00915582
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                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                              Human secreted protein #7
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KOMATSOULIS G A.
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BIRSE C E.
SOPPET D R.
OLSEN H S.
MOORE P A.
WEI P.
EBNER R.
DUAN D R.
SHI Y.
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FISCELLAM.
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RUBEN S M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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17-JAN-2001;
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Fiscella M,
                                                                                                                                                                                                                                                                                                                                05-NOV-2002
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(NIJJ/)
(RUBE/)
(BARA/)
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(BIRS/)
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(MOOR/)
(WEIP/)
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(DUAN/)
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                            ETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLEDFQPAAASE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a new method of detecting the presence of 30664188 antigen in a sample. The invention is useful for detecting the presence of 30664188 in a biological sample (e.g. blood or its component originating from a mammal, preferably human), and for contributing to diagnosis of cancer in a subject. The present amino acid sequence represents a human FCTR protein, as described in the methods of the invention
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100.0%; Pred. No. 1e-188;
iive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                    30664188 antigen; blood; cancer; human; FCTR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 11-13; 177pp; English.
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                                                                                                                                                                              ABG78502 standard; protein; 370 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lichenstein H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-NOV-2000; 2000US-00715332
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Best Local Similarity 100.0
                                                                                            DCICSSRPPR 370
                                                                        DCICSSRPPR 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andrews D,
                                                                                                                                                                                                                                                                        protein.
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                                                                                                                                                                                                                                                                        Human FCTR 1
                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                          15-NOV-2002
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                                        301
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                                                                                        The invention relates to an isolated nucleic acid molecule which encodes a human secreted protein. The sequences are useful for diagnosing or diagnosing a succeptibility to a pathological condition in a subject comprising determining the presence or absence of a mutation in the DNA or expression of the protein. The sequences are useful for identifying a binding partner to the protein comprising contacting the protein with a condition partner of the protein comprising contacting the protein with a condition goartner effects an activity. The DNA and protein sequences are used for preventing, treating contacting whether the binding partner effects an activity. The DNA and protein sequences are used for preventing, treating confidence or ameliorating a medical condition such as an autoimune disease (e.g. afibrinogenaemia, haemophilia), blood platelet disorders (e.g. sarcoidosis, Sezary conformed), neurodegenerative disorders (e.g. Alzheimer's disease, kidney infarction), cardiovascular disorders (e.g. renal vein thrombosis, kidney infarction), cardiovascular disorders (e.g. renal vein thrombosis, kidney disorders (e.g. thyrobosics), reproductive disorders (e.g. cardiac arreet, carcinos), assular disorders (e.g. aneurysm, ischaemia), respiratory disorders (e.g. aneurysm, ischaemia), aneurodescence acromedally, thyrotoxicosis), reproductive disorders (e.g. genorites), anorchia), gastrointestinal disorders (e.g. genorites), anorchia), gastrointestinal disorders (e.g. genorites), anorchia) and cancer. Carcinosis), infectious diseases (e.g. polio, rubella) and cancer.
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  diabetes, asthma, psoriasis, Parkinson's and Alzheimer's.
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100.0%; Pred. No. 1e-188;
iive 0; Mismatches 0
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Best Local Similarity
Matches 370; Conserv
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The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, disostured (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoistic disorders, neural disorders (e.g. Alzheimer's, haematopoistic syndrome, Jacob disease, encephalomyalitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention
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                                digestive disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinfilammatory; antiulcer; immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic; osteopathic; antiarthritic.
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serum albumin; HSA; cancer; reproductive disorder;
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100.0%; Pred. No. 1e-188;
ive 0; Mismatches 0;
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25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
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for reducing metastasis of prostate cancer cells to bone in
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Matches 370, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method for reducing proliferation of or extracellular matrix production by a cell in a mammal. The method comprises administering to the mammal a composition comprising a therapeutically effective amount of a zvegf4 antagonist chosen from activation, and mitogenically inactive, receptor-binding variants of zvegf4. Zvegf4 (also called PDGF-D) is a multi-domain protein that is structurally related to placelet derived growth factor (PDGF) and vascular endothelial growth factors (VEGF). Zvegf4 has cytostatic, nephrotropic, hepatotropic, antifilammatory, osteopathic and antiarthritic activities. The method is useful for reducing proliferation of mesangial, epithelial, endothelial, smooth muscle, fibroblast,
                                                                                                                                                                                                                                                fibroproliferative disorder; PDGF-D; platelet derived growth factor; PDGF, vascular endothelial growth factor; VBGF; cytostatic; nephrotropic; prostate tumour; prostate cancer; glomerulonephritis; lupus nephritis; prostate cancer; glomerulonephritis; lupus nephritis; diabetic glomerulosclerosis; renal arteriosclerosis; nephrotic syndrome; chronic active hepatitis; cirrhosis; osteopetrosis; osteosclerosis; hyperostosis; osteoarthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 osteoblast, osteoclast, neuronal, stromal, stellate or interstitial cells in a mammal, in particular proliferation of prostate tumour cells, and for reducing extracellular matrix production by a cell in a mammal suffering from a fibroproliferative disorder of kidmey, bone or liver. In particular it is useful for reducing stellate cell activation. The method
cell in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reducing proliferation or extracellular matrix production by a cell in a mammal, useful for treating fibroproliferative disorders of bone, liver and kidney, comprises administering a zvegf4 antagonist.
                                                                                                                                                                                                                                        zvegf4; cell proliferation; extracellular matrix production;
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GILBERTSON D G
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(TOPO/) TOPOL
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mammal and for treating a fibroproliferative disorder of kidney, liver or bone in a mammal. Fibroproliferative disorder of the kidney include, glomerulonosphritis, diabetic glomerulosclerosis, lupus nephritis, ronal arteriosclerosis and nephrotic syndrome, disorders of the liver include chronic active hepartits and many other types of cirrhosis, and disorders of the bone include osteopetrosis, hyperostosis, osteosclerosis, osteosclerosis, osteosclerosis, The present sequence represents human zvegf4, which is used in an example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MHRLIFVYTLICANFCSCRDTSATFQSASIKALRNANLRRDESNHLTDLYRRDETIQVKG
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//noce="Specifically claimed in claim 7"
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100.0%; Pred. No. 1e-188;
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whuman, growth factor homologue, zvegf4, fibroblast, smooth muscle cell, cell-surface platelet-derived growth factor alpha receptor; pDGF; whill-thickness skin wound; female reproductive tract; duodenal ulcer, prolonged bleeding; periodontal disease; tissue adheaive; liver damage; revasculariaation; healing tissue; liver disease; CPC; CHN; cirrhosis; chronic active hepatitis; hepatic chronic passive congestion; stroke; central hemorrhagic necrosis; hepatic chronic passive congestion; stroke; central vein thrombosis; cardiac sclerosis; new vessel formation; portal vein thrombosis; new vessel formation; cran transplant; tissue grafting; peripheral neuropathy; spinal cord; sensory neurite outgrowth; brain damage; head injury; paralysis; spinal injury; neurodegenerative disease; diabetic retinopathy; psocialis; scleroderma; keloid; liver fibrosis; psorlasis; wroliferative vascular discorder; ocular neovascularisation; inflammatory disorder; neuroderic creation; chamacoid arthritis; vasculogenesis; mervodes system disorder; cytostatic; paparents; concer; conc
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           181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMY 240
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                                                                               241 LDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVO
241 LDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQ
                                                                                                                                                                                                                                       301 RCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor homologue, zvegf4.
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99US-0142576P.
99US-0161653P.
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רבי West JW;
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N-PSDB; ABX93177.
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07-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated growth factor analogue ZVEF4 proteins for pharmaceutical composition as, e.g. therapeutic agents, diagnostic agents, and research tools and reagents, includes polypeptides from amino acid residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDESNHLTDLYRRDETIQVKG 60
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/note= "Specifically claimed in claim 5" 250. .370
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                                                                                                                                                           claim 2"
                                                                                                                                                                                                                                   /note= "Specifically claimed in claim 1"
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   250. .370 / note= "Specifically claimed in 250. .370 / note= "Specifically claimed in 7note= "Specifically claimed in 258. .370
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10-NOV-1999; 99US-0164463P.
04-FEB-2000; 2000US-0180169P.
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N-PSDB; ACA64109.
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The present invention relates to the isolation of a growth factor homologue referred to as zvegf3, and the polynucleotide sequence encoding it. The zvegf3 polypeptide is useful for stimulating the growth of fibroblasts or smooth muscle cells, or for activating the growth of platelet-derived growth factor (PDGF) alpha receptor. The zvegf3 coll-surface polypeptide is useful as a PDGF alpha receptor agonist and thus is useful cor treating full-thickness skin wounds, female reproductive tract and duodenal ulcers. The polypeptide is also useful fer an additive in tissue adhesives for promoting revascularisation of healing tissue. The zvegf3 polypeptide is also useful for treating liver damage including damage due congestion (CPC), central hemorrhagic necrosis, hepatic chronic passive congestion (CPC), central hemorrhagic necrosis, hepatic chronic passive congestion (CPC), central hemorrhagic necrosis, cardiac sclerosis, and many types of thrombosis, portal vein thrombosis, cardiac sclerosis, and many types of cirrhosis. The polypeptide is useful for enhancing expansion and mobilisation of endothelial precursor stem cells. Creating and circhemia, organ transplants, wound healing, and circhemia is useful for treating peripheral neuropathies by increasing spinal cord and sensory neurite outgrowths consequence treatment for the regeneration of neurite outgrowths consequence treatment for the regeneration of neurite outgrowths consed by spinal injuries. Application may also be made in treating neurodegenerative diseases (e.g. multiple sclerosis, Alzheimer's disease, (clinopathy, psoriasis, and paralysis caused by spinal injuries. Application may also be made in treating consequence of the readence of sclerosis, and glomerulosclerosis, Alzheimer's diseases (e.g. multiple sclerosis, Alzheimer's diseases (e.g. multiple sclerosis, Alzheimer's diseases (e.g. multiple sclerosis, Alzheimer's diseases) and plantal provascularisation the merovascularisation that provascularisation that provascularisation, and provascularisation, psoriasis, cancer, impaired or excessive vasculogenesis or angiogenesis, and diseases of the nervous system. The present sequence represents human

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; Sequence 2, Application US/09540224
; Patent No. 646513
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
                                                                                                                                 APPLICANT: Gao, Zeren
APPLICANT: Gao, Zeren
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-60
CURRENT APPLICATION NUMBER: U5/09/457,066
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: 7370
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100.0%; Pred. No. 1.2e-197;
ive 0; Mismatches 0;
ALIGNMENTS
                                                                                   Sequence 37, Application US/09457066
Patent No. 6432673
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Best Local Similarity 100.
Matches 370; Conservative
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ORGANISM: Homo sapiens
                                                                                                                      GENERAL INFORMATION:
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US-09-457-066-37
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APPLICANT: Gilbert, Teresa
APPLICANT: Gilbert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Bepgard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2.
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100.0%; Pred. No. 1.2e-197;
ive 0; Mismatches 0;
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CURRENT FILING DATE: 2000-03-31
EARLIER APPLICATION NUMBER: US 60/180,169
EARLIER FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 9
SUFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 370
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; Patent No. 6495668
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100.0%;
Best Local Similarity 100.0%;
Matches 370; Conservative 0
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Best Local Similarity 100.
Matches 370; Conservative
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US-09-564-595D-2
                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-540-224-2
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TYPE: PRT
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TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMY
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GEMEMAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Topouzis, Stavros
APPLICANT: Topouzis, Stavros
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: DISORDERS
TITLE OF INVENTION: DISORDERS
TITLE OF INVENTION: DISORDERS:
CURRENT APPLICATION NUMBER: US 60/235,295
PRIOR APPLICATION NUMBER: US 60/235,295
PRIOR PILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 1999-18-04
PRIOR PILING DATE: 1999-11-10
PRIOR PILING DATE: 1999-11-10
PRIOR PILING DATE: 1999-11-10
PRIOR PILING DATE: 1999-11-10
SRIOR PILING DATE: 1999-13,250
NUMBER OF SEQ ID NOSS: 13
SOFTWARE: FRASESEQ for Windows Version 3.0
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100.0%; Pred. No. 1.2e-197;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09808972
Patent No. 6630142
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 370; Conservative
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US-09-808-972-2
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ORGANISM:
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llarity 100.0%; Pred. No. 1.2e-197;
Conservative 0; Mismatches 0; Indels 0
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Pacent No. 6528050
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertgon, Debra G.
APPLICANT: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-60C1
CURRENT APPLICATION NUMBER: US/09/541,752
PRIOR PILING DATE: 2000-01-31
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 37
LENGTH: 370
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 370; Conserv
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TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, TITLE OF INVENTION: THEREFOR, AND USES THEREOF FILE REPERENCE: Ulf Entrason et al 1064-44833 CURRENT APPLICATION NUMBER: US/09/438,046 CURRENT PILING DATE: 1999-11-10 EARLIER APPLICATION NUMBER: 60/107,852 EARLIER FILING DATE: 1998-11-10 EARLIER FILING DATE: 1999-10-18 EARLIER PILING DATE: 1999-08-26 EARLIER FILING DATE: 1999-08-26 EARLIER FILING DATE: 1999-08-26 EARLIER FILING DATE: 1999-08-26 EARLIER FILING DATE: 1999-06-26 EARLIER FILING DATE: 1999-06-26 EARLIER FILING DATE: 1999-06-56 EARLIER FILING DATE: 1999-10-04 EARLIER FILING DATE: 1999-10-05 EARLIER FILING EARLIER FILING DATE: 1999-10-05 EARLIER FIL
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Patent No. 6814965

GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Sheepard, Christopher S.
APPLICANT: Sheepard, Paul O.
APPLICANT: Sheepard, Rimberly E.
APPLICANT: Sheepard, Faul O.
CURRENT EOF INVENTION: GROWH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-60

CURRENT FILNG DATE: 2002-05-02

CURRENT FILNG DATE: 2002-05-02
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Matches 370; Conservative
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US-10-139-583-37
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US-09-438-046-8
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                                                                                                                                                                                                                                               Sequence 5, Application US/09823033
Patent No. 6663870
GENERAL INFORMATION:
APPLICANT: Hart. Charles E.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
TITLE OF INVENTION: LIGAMENT AND CARTILAGE
FILE REFERENCE: 00-12
CURRENT APPLICATION NUMBER: US/09/823, 033
CURRENT PILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows Version 3.0
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100.0%; Pred. No. 1.2e-197,
iive 0; Mismatches 0;
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APPLICANT: AASE, Karin
APPLICANT: LEE, Xuri
APPLICANT: PONTN, Annica
APPLICANT: UUTELA, Marko
APPLICANT: UTTALO, Kari
APPLICANT: GESTWAN, Arne
APPLICANT: HELDIN, Carl-Henrik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 370; Conservative
                                                                                                      DCICSSRPPR 370
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CORGANISM: Homo sapiens
US-09-823-033-5
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US-09-823-033-5
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US-09-438-046-8
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      61 NGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRYDFVEVEDEDIS 120
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APPLICANT: BASE, Karin
APPLICANT: BASE, Karin
APPLICANT: BELKESON, Ulf
APPLICANT: BELKESON, Ulf
APPLICANT: BELKESON, Ulf
APPLICANT: UUTELA, Marko
APPLICANT: UUTELA, Marko
APPLICANT: UUTELA, Marko
APPLICANT: UUTELA, Kari
APPLICANT: HELDIN, Carl-Henrik
TILLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D,
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D,
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REPERENCE: Ulf Ethksson et al 1064-44833
CURRENT APPLICATION NUMBER: 60/107,852
EARLIER FILING DATE: 1999-11-10
EARLIER FILING DATE: 1999-11-28
EARLIER FILING DATE: 1999-12-28
EARLIER FILING DATE: 1999-08-26
EARLIER FILING DATE: 1999-08-26
EARLIER FILING DATE: 1999-10-05
EARLIER FILING DATE: 1999-10-05
EARLIER FILING DATE: 1999-10-05
MUMBER: OF SEQ ID NOS: 1
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Best Local Similarity 100.0%; Pred. No. 1.2e-171;
Matches 322; Conservative 0; Mismatches 0;
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; Sequence 6, Application US/09438046
; Patent No. 6706687
; GENERAL INPORMATION:
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US-09-438-046-6
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APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING TITLE OF INVENTION: KIDNEY FUNCTION
FILE REFERENCE: 00-100
CURRENT APPLICATION NUMBER: US/10/039,847A; PILING DATE: 2002-06-17
PRIOR FILING DATE: 2002-10-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
: SEQ ID NO 2.
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100.0%; Score 1994; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.2e-197;
Matches 370; Conservative 0; Mismatches 0;
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100.0%; Score 1994; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.2e-197;
Matches 370; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOTUMARE: FagtSEQ for Windows Version 3.0
SEQ ID NO 37
LENGTH: 370
TYPE: PRT
ORGANISM: HOMO Bapiens
US-10-139-583-37
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US-10-039-847A-2
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                                                                                                                241 NVVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 300
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PESWQEDLENMYLDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLA
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                                                                                                                                                                                                                                                                                           APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Hart, Charles E.
TITLE OF INVENTION: METHODS POR PROMOTING GROWTH OF BONE,
TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4;
FILE REFERENCE: 00-28
CURRENT APPLICATION NUMBER: US/09/540,224
CURRENT FILING DATE: 2000-03-31
EARLIER APPLICATION NUMBER: US 60/180,169
EARLIER FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 370
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85.1%; Pred. No. 4.8e-171;
iive 25; Mismatches 30;
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                                                                                                                                                                                                                                                      Sequence 4, Application US/09540224
Patent No. 6468543
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Best Local Similarity 85.1<sup>§</sup>
Matches 315; Conservative
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US-09-540-224-4
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RESULT 12 US-09-564-595D-53

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APPLICANT: Hart, Charles E.
APPLICANT: TOPOUZIS, STAVOS
TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: 00-79
CURRENT APPLICATION NUMBER: US/09/808,972
CURRENT APPLICATION NUMBER: US 60/235,295
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
Sequence 53, Application US/09564595D; Patent No. 649568
GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Gilbert, Teresa
APPLICANT: Bieppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REPERENCE: 99-19
CURRENT RILING DATE: 2000-05-03
FRIOR APPLICATION NUMBER: US/09/564,595D
CRRENT FILING DATE: 1999-05-03
FRIOR APPLICATION NUMBER: US 09/304,216
FRIOR APPLICATION NUMBER: US 09/304,216
FRIOR APPLICATION NUMBER: US 60/164,463
FRIOR APPLICATION NUMBER: US 60/164,463
FRIOR FILING DATE: 1999-11-10
FRIOR FILING DATE: 1999-10-03
SEQ ID NO 53
SEQ ID NO 53
LENGTH: 370
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85.1%; Pred. No. 4.8e-171;
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Patent No. 6630142
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61 NGHVQSPRFPNSYPRNLLLTWWLRSQEKTRIQLSFDHQFGLEEAENDICRYDFVEVEEEV 120
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                                                                                              NGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRYDFVEVEDIS 120
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                      61 DFVEVEDISETSTIIRGRWCGHKEVPPRIKKSRINQIKITFKSDDYFVAKPGFKIYYSLLE
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US-09-564-595D-56

Sequence 56, Application US/09564595D

Patent No. 649568

GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOWOLOG ZVEGF4
FILE REFERENCE: 99-10

CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 09/304,216

PRIOR PILING DATE: 1999-05-03
PRIOR PILING DATE: 1999-05-03

PRIOR FILING DATE: 1999-05-04

NUMBER OF SEC ID NOS: 57

SEC ID NO 56

LENGTHA: 317
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Best Local Similarity
Matches 263; Conserv
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Patent No. 6827938

GENERAL INFORMATION:
TOTALE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING
TITLE OF INVENTION: KIDNEY FUNCTION
TITLE OF INVENTION: KIDNEY FUNCTION
CURRENT APPLICATION NUMBER: US/10/039,847A
CURRENT APPLICATION NUMBER: US 60/244,479

PRIOR FILING DATE: 2000-10-30
                                                                                                                                                                                                                                                                           Length 370;
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85.1%; Pred. No. 4.8e-171;
ive 25; Mismatches 30; Indels
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85.1%; Pred. No. 4.8e-171;
1ive 25; Mismatches 30;
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FQSLERQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 370
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 370
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Best Local Similarity 85.1
Matches 315, Conservative
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Best Local Similarity 85.1
Matches 315; Conservative
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TYPE: PRT
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181 WQEDLENMYLDTPRYRGRSYHDRKSKVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDT 240
                                                                          241 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRP---KTGVRGLHKSLT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSL-L 170
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                                                                                                                                                                                                                                                                                                       GENERAL INC. 0423000

GENERAL INC. 0423000

APPLICANT: Gilbert Teresa

APPLICANT: Sheppard, Paul O.

TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4

FILE REPERENCE: 99-19

CURRENT APPLICATION NUMBER: US/09/564,595D

CURRENT FILING DATE: 2000-05-03

PRIOR PILING DATE: 1999-05-03

PRIOR APPLICATION NUMBER: US 09/304,216

PRIOR APPLICATION NUMBER: US 06/164,463

PRIOR APPLICATION NUMBER: US 60/164,463

PRIOR FILING DATE: 1999-11-10

PRIOR APPLICATION NUMBER: US 60/180,169

PRIOR APPLICATION NUMBER: US 60/180,169

PRIOR APPLICATION NUMBER: US 60/180,169

PRIOR FILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 57

LUMBER OF SEQ ID NOS: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: fusion polypeptide US-09-564-595D-55
                                                                                                                                                                                                                                                                    Sequence 55, Application US/09564595D
Patent No. 6495668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                       DIQLDHHERCDCIC 364
                                                                                                                                                                        298
                                                                                                                                   351
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RESULT 17 US-09-564-595D-57

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165 RWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRT 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 RDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 DFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 DFQPAAASETNWESVTSSISGVSYNSPSVTDPT-LIADALDKKIAEFDTVEDLLKYFNPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 SWQEDLENMYLDTPRYRGRSY-HDRKSK-VDLDRLNDDAKRYSCTPRNYSVNIREELKLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 54.9%; Score 1095; DB 4; Length 3 Best Local Similarity 67.4%; Pred. No. 1e-104; Matches 213; Conservative 26; Mismatches 55; Indels
                                                            APPLICANT: HILEGA TELES E.
APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
SPRIOR FILING DATE: 2000-05-04
SOFTWARE FRALES FRALES FOR TOWNS: 57
SOFTWARE FRALES FRALES FOR TOWNS: 57
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282 LTDVALEHHEECDCVC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
Patent No. 6495668
GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-564-595D-54
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74 PRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCG 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 VEDLLKYFNPESWQEDLENMYLDTPRYRGRSY-HDRKSK-VDLDRLNDDAKRYSCTPRNY 277
                                                                                                                                                                                                                                                                                244 PRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 LEEAENDICRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAK 160
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                                                                                                                                                                                                                          73
                                                                                                                                                                                                      14 ESVTSSVSGYPYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENYLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 ESNHLIDLYRRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHS-QENTRIQLVFDNQFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 PGFKIYYSLLEDFQPAAASETNWESVTSSISGVSYNSPSVTDP-TLIADALDKKIAEFDT
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                                                           Length 200;
                                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Rimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 99-607
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
                                                           Score 982; DB 4;
Pred. No. 2.7e-93;
1; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                338 IKRRGRAKTMALVDIQLDHHERCDCIC 364
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                                                              49.2%;
96.8%;
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Best Local Similarity 45.3%
Matches 148; Conservative
                                                           Query Match
Best Local Similarity 96.8
Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Mus musculus US-09-457-066-43
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Patent No. 6432673
GENERAL INFORMATION:
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US-09-457-066-43
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TYPE: PRT
        US-09-438-046-4
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                                                                                                                                                                                                                                                                                                                                                                                    53 DETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHS-QENTRIQLVFDNOFGLEEAENDICRY 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSL-L 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 DFVEVEEBSDGT--1LGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVM 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 EDFOPAAASETNWESVTSSISGVSYNSPSVTDPT-LIADALDKKIAEFDTVEDLLKYFNP 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 ESWOEDLENMYLDTPRYRGRSY-HDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                289 NVVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 348
                                                                                                                                                                                                                                                                                                                                                                                                                      2 ERIITVSTWGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIOLTFDERFGLEDPEDDICKY
                                                                                                                                                                                                                                                                                                                                   25; Gaps
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                                                                                                                                                                                                                                                                          Query Match 53.2%; Score 1061.5; DB 4; Length 302; Best Local Similarity 64.0%; Pred. No. 3e-101; Matches 206; Conservative 36; Mismatches 55; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: ERIKSSON, U1f
APPLICANT: ERIKSSON, U1f
APPLICANT: AASE, Karin
APPLICANT: PONTN, Annica
APPLICANT: PONTN, Annica
APPLICANT: HILLA, Marko
APPLICANT: HILLA
APPLICANT: HILLA
APPLICANT: HILLA
APPLICANT: 1999-11-10
EARLIER APPLICATION NUMBER: 60/107,852
EARLIER APPLICATION NUMBER: 60/103,997
EARLIER FILING DATE: 1999-12-28
EARLIER PILING DATE: 1999-10-04
EARLIER FILING DATE: 1999-10-05
EARLIER PILING DATE: 1999-10-05
EARLIER FILING DATE: 1999-10-05
EARLIER PILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 54
LENGTH: 302
                                                                                                                                                            FEATURE:

/ OTHER INFORMATION: fusion polypeptide

US-09-564-595D-54
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US-09-438-046-4
; Sequence 4 Application US/09438046
; Patent No. 6706687
                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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Search completed: November 10, 2005, 09:37:14 Job time : 46.9627 secs

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Sequence 2, Appliseduence 2, Appliseduence 4, Appliseduence 5, Appliseduence 6, Appliseduence 6, Appliseduence 7, Appliseduence 5, Appliseduence 6, Appliseduence 6, Appliseduence 7, Appliseduence 18, Appliseduence 18
Sequence 5, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 1482, Ap
Sequence 182, Ap
Sequence 3, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
                                                                ; Search time 169.296 Seconds (without alignments) 914.442 Million cell updates/sec
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       GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-808-972-2
US-09-915-582-56
US-09-876-813-2
US-10-08-623-8
US-10-10-13-583-37
US-10-039-847A-2
US-10-039-847A-2
US-10-258-557-2
                                                                                                                                                                                      hits satisfying chosen parameters:
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Maximum Match 100%
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seq length: 200000000
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100.0%; Pred. No. 1.7e-167;
iive 0; Mismatches 0;
US-10-147-517-186
US-10-147-526-186
US-10-121-041-186
US-10-121-043-186
US-10-121-043-186
US-10-123-215-186
US-10-123-902-186
US-10-123-909-186
US-10-123-909-186
US-10-123-909-186
US-10-123-909-186
US-10-123-910-186
US-10-124-817-186
US-10-124-817-186
US-10-125-922-186
US-10-125-922-186
US-10-125-922-186
US-10-125-922-186
                                                                                                                                                                                                                                                        APPLICANT: Hart, Charles E.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHODS FOR PROMOTING GROW
TITLE DE INVENTION: LIGAMENT AND CARTILAGE
FILE REFERENCE: 00-12
CURRENT APPLICATION NUMBER: US/09/823,033
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 370
                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                             ; Sequence 5, Application US/09823033 ; Patent No. US20020004225A1 ; GENERAL INFORMATION:
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  DCICSSRPPR 370
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, ORGANISM: Homo sapiens
US-09-823-033-5
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Best Local Similarity
 US-09-823-033-5
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                                                                    APPLICANT: Hart, Charles E.
APPLICANT: Topouzis, Stavros
APPLICANT: Topouzis, Stavros
APPLICANT: Topouzis, Stavros
APPLICANT: Topouzis, Stavros
TITLE OF INVENTION: Debra G.
TITLE OF INVENTION: DISORDERS
TITLE OF INVENTION: DISORDERS
TITLE OF INVENTION: DO OF TREATING FIBROPROLIFERATIVE
TITLE OF INVENTION: DO OF TREATING FIBROPROLIFERATIVE
TITLE OF INVENTION: DO OF TREATING FIBROPROLIFERATIVE
TITLE OF INVENTION NUMBER: US 60/235,295
PRIOR PELICATION NUMBER: US 60/235,295
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR PLING DATE: 2000-02-04
PRIOR PLING DATE: 1099-11-10
PRIOR FILING DATE: 1099-11-10
PRIOR PLING DATE: 1999-11-10
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100.0%; Pred. No. 1.7e-167;
7ative 0; Mismatches 0;
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US-09-915-582-56
Sequence 56, Application US/09915582
Sequence 56, Application US/09915582
GENERAL INFORMATION:
GENERAL INFORMATION:
1 TILLE OF INVENTION: 17 Human Secreted Proteins
FILE REFERENCE: PS72391
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SOFTWARE: FastSEQ for Windows Version 3.0
Sequence 2, Application US/09808972
Patent No. US20020064832A1
GENERAL INFORMATION;
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                                                                                                                                      Length 370;
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                                                                                                                                  100.0%; Score 1994; DB 11;
100.0%; Pred. No. 1.7e-167;
ive 0; Mismatches 0;
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TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
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US-09-833-245-1482
Schence 1482, Application US/09833245
Publication No. US20040010134A1
GENERAL INFORMATION:
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Matches 370; Conservative
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SEQ ID NO 1482
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                                                  TYPE: PRT
ORGANISM: Homo sapiens
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SEQ ID NO 2
LENGTH: 370
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ORGANISM:
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Pred. No. 1.7e-167;
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Fublication No. US20040002140A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
FUBPLICANT: GIADETT, TERESS
APPLICANT: Hart, Charles E.
APPLICANT: Happard, Paul O.
TITLE OF INVENTION: GROWTH PACTOR HOMOLOG ZVE
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/876,813
CURRENT FILING DATE: 2001-06-06
FRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-05-03
FRIOR FILING DATE: 1999-11-10
FRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FASLSEQ FOR WINGONS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                  CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION UNDRER: PCT/USO1/01431
PRIOR APPLICATION UNDRER: PCT/USO1/01431
PRIOR PLING DATE: 2000-01-17
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-12
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PALENTIN Ver. 2.0
LENGTH: 370
  CURRENT APPLICATION NUMBER: US/09/915,582
CURRENT FILING DATE: 2001-07-27
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 370; Conservative 0
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, ORGANISM: Homo sapiens
US-09-915-582-56
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Db 61 NGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEBAENDICRYDFVEVEDIS 120 Qy 121 ETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVARRGFKIYYSLLEDFQPAAASE 180 121 ETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVARRGFKIYYSLLEDFQPAAASE 180 Qy 181 TNWESVTSSISGVSYNSPSYTDFTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENNY 240 181 TNWESVTSSISGVSYNSPSYTDFTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENNY 240 241 LDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFPRCLLVQ 300 Qy 241 LDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFPRCLLVQ 300 Db 241 LDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFPRCLLVQ 300 QY 301 RCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360 QY 361 DCICSSRPPR 370 Db 361 DCICSSRPPR 370	RESULT 6 (S-10.06-621-8) Sequence a, Application US/10086623 Sequence a, Application US/10086623 Sequence a, Application US/10086623 Sequence a, Application US/10086623 Septic Mark Marker Control Cont

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                   APPLICANT: ALIMAN, ARNA
APPLICANT: ALIMAN, ARNA
APPLICANT: GESTWAN, ARNA
APPLICANT: HELDIN, CATLHENTIK
TITLE OF INVENTION, DATELET DERIVED GROWTH FACTOR D, DNA
FILE REFERENCE: 106444833C2
CURRENT APPLICATION NUMBER: US/10/260,539
CURRENT APPLICATION NUMBER: US/00-10-01
PRIOR FILING DATE: 2000-03-04
PRIOR FILING DATE: 1998-11-10
PRIOR PELLOR DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 60/113,997
PRIOR APPLICATION NUMBER: US 60/150,604
PRIOR APPLICATION NUMBER: US 60/157,108
PRIOR FILING DATE: 1999-10-04
PRIOR FILING DATE: 1999-10-04
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 2000-10-19
NUMBER OF SEQ ID NOS: 42
SEGTWARE PLEING DATE: 2000-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 1994; DB 14; Best Local Similarity 100.0%; Pred. No. 1.7e-167; Matches 370; Conservative 0; Mismatches 0;
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US-10-264-361-5
; Sequence 5, Application US/10264361
; Boblication No. US20330087870A1
; GENERAL INFORMATION:
; APPLICANT: Glibertson, Debra G.
; TILE GF INVENTION:
; FILE REFERENCE: 00-53
; CURRENT APPLICATION NUMBER: US/10/264,361
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ORGANISM: Homo sapiens
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61 NGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRXDFVEVEDIS 120
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| Sequence 2, Application US/10039847A
| Publication No. US20020183273A1
| GENERAL INFORMATION:
| APPLICANT: Hart, Charles E.
| APPLICANT: Hart, Charles E.
| APPLICANT: Topouzis, Stavros
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING TITLE OF INVENTION: COMPOSITIONS FUNCTION FILE REFERENCE: 00-100
| CURRENT APPLICATION NUMBER: US/10/039,847A |
| PRIOR FILING DATE: 2002-06-17 |
| PRIOR FILING DATE: 2000-10-30 |
| NUMBER OF SEQ ID NOS: 10 |
| SOFTWARE: FastSEQ for Windows Version 3.0 |
| LENGTH: 370
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US-10-260-539-8
Schoole B, Application US/10260539
Publication No. US20030073637A1
GENERAL INPORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: LI, Xuri
APPLICANT: PONTEN, Annica
APPLICANT: PONTEN, Annica
APPLICANT: UUTELA, Marko
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ORGANISM: Homo sapiens
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   61 NGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFCLEEAENDICRYDFVEVEDIS
                                                                                                                                                        121 ETSTIIRGRWCGHKEVPPRIKSRINQIKIIFKSDDYFVAKPGFKIYYSLLEDFOPAAASE
                                                                                                                                                                                                     1 MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDESNHLTDLYRRDETIQVKG
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Sequence 2, Application US/10226559;
Publication No. USCO30105015A1
GENERAL INFORMATION:
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHODS FOR PROWOTING GROWTH OF BONE,
TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4;
TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4;
TITLE OF INVENTION: MARBER: US/10/226,559
CURRENT APPLICATION NUMBER: US/09/540,224
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-04
NUMBER: OF SEQ ID NOS: 9
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 370
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US-10-226-559-2
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Pred. No. 1.7e-167;
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100.0%; Pred. No. 1.7e-167;
ive 0; Mismatches 0;
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APPLICANT: Gonzalez-DeWhitt, Patricia
APPLICANT: Gonzalez-DeWhitt, Patricia
APPLICANT: Hammond, Lisa
APPLICANT: Lu, Jirong
APPLICANT: Na, Songqing
APPLICANT: Na, Eric
APPLICANT: Na, Eric
APPLICANT: Natcher, Derrick
TITLE OF INVENTION: TREATING MUSCULOSKELETAL DIS
FILE REFERENCE: X-143298
CURRENT FILING DATE: 2002-10-23
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
                                                                                                                                                                                                    Query Match
100.0%; Score 1994;
Best Local Similarity 100.0%; Pred. No. 1.7
Matches 370; Conservative 0; Mismatches
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: US/09/695,121
PRIOR FILING DATE: 2000-10-23
NUMBER OF SEC 1D NOS: 18
SOFTWARE: FastSEQ for Windows Vergion 3.0
SEQ ID NO 5
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
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Publication No. US20030100502A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 370; Conservative
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; ORGANISM: Homo sapiens
US-10-258-557-2
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APPLICANT: Engrysus, communications applicant: Parence APPLICANT: Boldog, Ference APPLICANT: Yang, Meijia APPLICANT: Yang, Meijia APPLICANT: Yang, Meijia APPLICANT: Purgess, Catherine APPLICANT: Fernandes, Elma APPLICANT: Rittman, B. APPLICANT: Rittman, B. APPLICANT: Rittman, B. APPLICANT: Rittman, B. APPLICANT: Largochelle, William TITLE OF INVENTION: Treatment of Inflammatory Bowel Disease Using Growth TITLE OF INVENTION: Treatment of Inflammatory Bowel Disease Using Growth TITLE OF INVENTION NUMBER: US/10/011,364
CURRENT APPLICATION NUMBER: US/10/011,364
PRIOR PILING DATE: 2000-11-06
PRIOR PRILING DATE: 2001-11-06
PRIOR PRILING DATE: 2001-11-06
PRIOR PRILING DATE: 2001-11-06
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
IPMCMHL 370
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100.0%; Score 1994; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0;
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US-10-277-802-56

Sequence 56, Application US/10277802

Publication No. US20030190707A1

GENERAL INFORMATION:
TITLE OF INVENTION: 17 Human Secreted Protein
FILE REFERENCE: PS722P1

CURRENT APPLICATION NUMBER: US/10/277,802

CURRENT FILING DATE: 2002-10-23

PRIOR FILING DATE: 2001-07-27

PRIOR PILING DATE: 2001-07-27

PRIOR APPLICATION NUMBER: 09/915,582
     Jeffers, Michael
Shimkets, Richard
Prayaga, Sudhirdas
Boldog, Ferenc
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61 NGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRYDFVEVEDIS 120
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US-10-274-638-2
; Sequence 2, Application US/10274638
; Publication No. US20030109000A1
; GENERAL INFORMATION:
    APPLICANT: Moore, Margaret D.
; APPLICANT: Moore, Margaret D.
; TITLE OF INVENTION: DIMERIZED GROWTH FACTOR AND MATERIALS
; TITLE OF INVENTION: DAND METHODS FOR PRODUCING IT
FILE REPRENCE: 01-30
CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 06/346,117
PRIOR APPLICATION NUMBER: 2001-10-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FASUS Q for Windows Version 4.0
; SEQ ID NO : LENGTH: 370
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US-10-011-364-4
; Sequence 4, Application US/10011364
; Publication No. US20030153495A1
; GENERAL INFORMATION:
; APPLICANT: Lichengtein, Henry
                                                                                                                                                                      DCICSSRPPR 370
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-10-246-091-8
Sequence 8, Application US/10246091
Publication No. US20030203844A1
Bublication No. US20030203844A1
Bublicantion No. US2003020384A1
APPLICANT: Janson, Ann Marie
APPLICANT: Janson, Anne
APPLICANT: Schnazer, Anne
APPLICANT: Schnazer, Anne
APPLICANT: Zhao, Ming
TITLE OF INVENTYON: Treatment of Central Nervous System Disorders
TITLE OF INVENTYON: Treatment of Central Nervous System Disorders
CURRENT APPLICATION NUMBER: US/10/246,091
CURRENT APPLICATION NUMBER: 60/323,381
PRIOR FILING DATE: 2001-09-19
PRIOR PILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATEULIN VEY: 2.1
TYPE: PRT
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100.0%; Pred. No. 1.7e-167;
iive 0; Mismatches 0;
PRIOR FILING DATE: 2001-01-17
PRIOR PELLING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PALENTIN Ver. 2.0
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Matches 370; Conservative
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ORGANISM: Homo sapiens
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US-10-277-802-56
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                                                                                                                  Indels
Query Match
100.0%; Score 1994; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; I
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APPLICANT: Moore, Margaret D.
APPLICANT: Moore, Margaret D.
APPLICANT: Birks, Carl M.
TITLE OF INVENTION: MATERIALS AND METHODS FOR FILE REFERENCE: 01-33
CURRENT FLING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: 60/355,882
PRIOR APPLICATION NUMBER: 60/355,882
PRIOR APPLICATION NUMBER: 60/355,882
PRIOR APPLICATION NUMBER: 60/355,882
SRIGH FILING DATE: 2002-02-11
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 2, Application US/10365095; Publication No. US20030224488A1
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US-10-365-095-2
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                                    301 RCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQPEPGHIKRRGRAKTMALVDIQLDHHERC 360
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                                                                                                                                                                                                               Sequence 2. Application US/10606055
Publication No. US20040043027A1
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
TITLE OF INVENTION: MUMBER: US/10/606,055
CURRENT FILING DATE: 2003-06-25
PRIOR FILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 1999-14
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR PILING DATE: 1999-11-10
PRIOR PILING DATE: 1999-11-10
PRIOR PILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-105-03
NUMBER OF SEQ ID NOS: 13
SOFTWARR: PEASEEQ for Windows Version 3.0
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100.0%; Pred. No. 1.7e-167;
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ORGANISM: Homo sapiens
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APPLICANT: Boldoy, Ferenc L.
APPLICANT: Burgess, Catherine E.
APPLICANT: Fernandes, Elma
APPLICANT: Jeffers, Michael E.
APPLICANT: Lichenstein, Henry S.
APPLICANT: Peterson, Jeffrey
APPLICANT: Peterson, Jeffrey
APPLICANT: Rittman, Beth
APPLICANT: Shimkers, Juliette
APPLICANT: Shimkers, Juliette
APPLICANT: Shimkers, Richard A.
APPLICANT: Yang, Meijia
APPLICANT: Vang, Meijia
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Publication No. US20040006015A1
GENERAL INFORMATION:
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Sequence 5, Application US/10664432

Sequence 5, Application US/10664432

Publication No. US20040043031A1

GENERAL INFORMATION:

APPLICANT: Hart, Charles E.

APPLICANT: Gilbertson, Debra G.

TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,

TITLE OF INVENTION: LIGAMENT AND CARTILAGE

FILE REFRENCE: 00-12

CURRENT APPLICATION NUMBER: US/10/664,432

CURRENT PILING DATE: 2003-09-19

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 5

LENGTH: 370

TYPE: RPT.

CREAT: 170

CREAT:
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dorsal-yentral pat
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Ra-reactive factor
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TSG-6 homolog PS4
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hyaluronate-bindin
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spinal cord-derive
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                                              November 10, 2005, 09:24:01; Search time 39.0683 Seconds (without alignments) 911.229 Million cell updates/sec
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                                                                                           1 MHRLIFVYTLICANFCSCRD.....DIQLDHHERCDCICSSRPPR 370
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      5.1.6
Compugen Ltd
                                                                                                                                              of hits satisfying chosen parameters:
                                                                                                                                283416 segs, 96216763 residues
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       GenCore version (c) 1993 - 2005
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Maximum Match 100%
Listing first 100 summaries
                                   - protein search, using sw model
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JC2218
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ALIGNMENTS

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Matches 321; Conservative
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Species: Homo sapiens (man)
C;Species: Solution: 2001
R;Hamada, T.; Ul-Tei, K.; Imaki, J.; Miyata, Y.
Bjochem: Biochban. 280, 733-737, 2001
A;Tile: Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-C/A;Reference number: JC7591; MUID:21092670; PMID:11162582
A;Reference number: JC7591; MUID:21092670; PMID:11162582
A;Residues: 1-370 AHA
A;Residues: 1-370 AHA
A;Residues: UNIPROT:Q9BWV5; UNIPROT:Q9GZP0; DDBJ:AB033832
C;Genetics:
A;Gene scdgf-B
F;1-17/Domain: secretory signal sequence #status predicted <SIG>F;1-17/Domain: secretory signal sequence #status predicted AFGE-F;2-170/Region: homologous to platelet-derived growth factor/vascular endothelial grow
F;22-2-370/Region: homologous to platelet-derived growth factor/vascular endothelial grow
F;22-370/Region: conserved motif #status predicted
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307592

spinal cord-derived growth factor-B precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004

R;Hamada, T: Jul-rei, K.; Imaki, J.; Miyata, Y.

Biochem. Biophys. Res. Commun. 280, 733-737, 2001

A;Title: Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-C/A;Contents: Fetal brain

A;Reference number: JC7591; MUID:21092670; PMID:11162582

A;Contents: Fetal brain

A;Accession: JC7592

A;Anolecule type: mRNA

A;Residues: 1-370 c+AMA>

A;Cross-references: UNIPROT:Q9EQT1; DDBJ:AB052170
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AjGene: scdgf-B
Fil-17/Domain: secretory signal sequence #status predicted <SIG>
Fil-17/Domain: secretory cord-derived growth factor-B #status predicted <MAT>
Fil-370/Prediction: CUB domain #status predicted
Fi272-370/Region: CUB domain #status predicted growth factor/vascular endothelial grow
Fi294-308/Region: conserved motif #status predicted
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: JC7998
R;Zhuo, Y.; Hoyle, G.W.; Zhang, J.; Morris, G.; Lasky, J.A.
Biochem. Biophys. Res. Commun. 308, 126-132, 2003
A;Title: A novel murine PDGF-D splicing variant results in significant differences: A;Reference number: JC7998; PMID:12890490
A;Reference number: JC7998
A;Rolecule type: mRNA
A;Residues: 1-370 <ZHU>
C;Comment: This protein is a potent mesenchymal cell mitogen and chemoattractant in C;Genetics:
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A;Introns: 42/2; 110/1; 170/2; 191/2; 258/2; 330/1; 334/2
C;Keywords: fibrosis; PDGF-D
                                                                                                                                                                                                    ; Score 1775; DB 2;
; Pred. No. 1.6e-126;
23; Mismatches 26;
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85.1%; Pred. No. 1.2e-123;
cive 25; Mismatches 30;
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A; Map position: 8p21-8p21

A; Map position: Qualizes hydrolysis of the carboxyl-terminal propeptide of collagen type C; Function:

A; Description: Catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type C; Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology; E C; Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl f; 1-22/Opmain: signal sequence #scatus predicted <SIG>
F; 33-822/Product: procollagen C-endopeptidase splice form HIS #status predicted <MAT>
F; 130-321/Domain: astacin homology <AST>
F; 32-491/Domain: Clr/Cls repeat homology <Clr?>
F; 551-594/Domain: Clr/Cls repeat homology <Clr?>
F; 551-587/Domain: Clr/Cls repeat homology <Clr?>
F; 591-700/Domain: Clr/Cls repeat homology <Clr?>
F; 91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 114,Active site: Glu #status predicted
F; 114/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession type: mknn
A;Molecule type: mknn
A;Residues: 703-823 <TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              procollagen C-endopeptidase (EC 3.4.24.19)
N;Alternate names: bone morphogenic protein
C;Species: Homo sapiens (man)
C;Date: 28-Mar-1998 #sequence_revision 09-A
C;Accession: A37278; A58788
R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; N
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A58788
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A;Rosidues: 1-702; EKRPALQPPRGRPHQLKFRVQKRNRTPQ' <WOZ>
A;Cross-references: GB:M22488; NID:g179499; PIDN:AAAS1833.1; PID:g179500
R;Takahara, K.; Lyons, G.E.; Greenspan, D.S.
J.Biol. Chem. 269. 32572-32578, 1994
A;Tatle: Bose morphogenetic protecin-1 and a mammalian tolloid homologue (mTld)
A;Reference number: A58788; MUID:95096114; PMID:7798260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 242, 1528-1534, 1988
A;Title: Novel regulators of bone
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                                                                                                        Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: GB:L35278;
                                                                                      Matches
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KLNGSITSPGWPKEYPPNKNCIWQLVAPTQYRISLQFD---FFETEGNDVCKWDFVEVRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lators of bone formation: molecular A37278; MUID:89072730; PMID:3201241
                                                                                                        9.7%;
28.7%;
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                                                                                                     Score 193; 1
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                                                                                 DB 1;
L.5e-06;
les 89;
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                                    procollagen C-endopeptidase (EC 3.4.24.19) precursor, N,Alternate names: bone morphogenic protein 1 (BMP1) C;Species: Homo sapiens (man) C;Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #tc;Accession: A37278; ES8788 R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.! Science 242, 1528-1534, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 134, 257-261, 1993
A;Title: Cloning and expression of cDNA encoding Xenopus
A;Reference number: JC2218; MUID:94085787; PMID:8262384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Maeno, M.; Xue, Y.; Wood, T.I.; Ong, R.C.; Kung, Gene 134, 257-261, 1993
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A; Title: Novel regulators of bone formation: molecular clones and A; Reference number: A37278; MUID:89072730; PMID:3201241
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A; Residues: 1-707 < MAE>
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N; Alternate names:
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Date: 30-Sep-1993 #sequence_revision 20-Aug-1994
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Similarity 42.5%;
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Pred. No. 2.2e-06;
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•
                                                               L.M.; Whitters,
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A;Cross-references: UNIPROT:P98070; GB:L12249; NID:g406540; PIDN:AAA16313.1; PID:g4065.2;Comment: This protein induces ectopic cartilage formation in vivo.
C;Gument: This protein induces ectopic cartilage formation in vivo.
C;Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology;
C;Keywords: beta-hydroxysasparagine; glycoprotein; hydrolase; metalloproteinase; zinc
C;Superfamily: procollagen C-endopeptidase; astacin homology;
C;Keywords: beta-hydroxysasparagine; glycoprotein; hydrolase; metalloproteinase; zinc
F;338-39/Region: complement lr/Is-like repeat
F;285-39/Domain: Clr/Cls repeat homology <ClR1>
F;398-510/Region: complement lr/Is-like repeat
F;398-510/Region: complement lr/Is-like repeat
F;398-50/Domain: GGF homology <CGR2>
F;514-550/Domain: GGF homology <GGF>
F;514-666/Region: complement lr/Is-like repeat
F;554-666/Region: complement lr/Is-like repeat
F;554-666/Region: complement lr/Is-like repeat
F;554-666/Region: complement lr/Is-like repeat
F;554-666/Region: complement lr/Is-like repeat
F;514-550/Domain: GGF homology <GCR3>
F;62,105,295,326/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;116,180,186,335/Binding site: zinc (His, His, His, Tyr) #status predicted
F;117/Active site: Glu #status predicted
                                                                            ISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFK 164
                                                                                                                                                                                                                                                       KGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRYDFVEVED 118
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A;Cross-references: UNIPROT:P13497; GB:M22488; NID:g179499; P1 R;Takahara, K.; Lyons, G.E.; Greenspan, D.S.
J. Biol. Chem. 269, 32572-32578, 1994
A;Title: Bone morphogenetic protein-1 and a mammalian tolloid A;Reference number: A58788; MUID:95096114; PMID:7798260
A;Accession: RGR7RR
                                                                                                                                                                                                                             A; Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;322-431/Domain: C1r/C1s repeat homology <C1R1>
F;435-544/Domain: C1r/C1s repeat homology <C1R2>
F;435-544/Domain: C1r/C1s repeat homology <C1R2>
F;551-587/Domain: EGF homology <EGF>
F;551-700/Domain: C1r/C1s repeat homology <C1R3>
F;91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
F;213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F;214/Active site: G1u #status predicted
F;565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
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  F;322-431/Domain: F;435-544/Domain:
                                               F;23-986/Product: procollagen C-endopeptidase tolloid-like F;130-321/Domain: astacin homology <astro-
                                                                                                                                                      A; Description: C; Superfamily:
                                                                                                                                                                                                                                                                                                                            A;Residues: 703-986 <TAK>
A;Cross-references: GB:L35279; NID:g619860;
                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRN
A: Residues: 703-986
                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A; Accession: B58788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Science 242, 1528-1534, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloi
N;Alternate names: bone morphogenic protein 1, tolloid-like
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A; Residues: 1-730 < WC
                                                                                                                                                                                                                                                       A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-702, 'EKRPALQPPRGRPHQLKFRVQKRNRTPQ'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: A37278; MUID:89072730; PMID:3201241
A;Accession: A37278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Novel regulators of bone formation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                 ;Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen;Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology;Keyworde: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication;1-22/Domain: signal sequence #status predicted (SIG)
                                                                                                                                                                                                                                                    ;Gene: GDB:BMP1; BMP-1
;Cross-references: GDB:125203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Homo sapiens (man)
Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change;
                                                                                                                                                                                                        Function
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRYDFVEVED 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLNGSITSPGWPKEYPPNKNCIWQLVAPTQYRISLQFD---FFETEGNDVCK/XDFVE
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Clr/Cls repeat homology Clr/Cls repeat homology
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                          homology <ClR1>
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No. 3.3
<C1R2>
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A;Gene: Bmp.1
C;Superfamily: procollagen C-endopeptidase; astac C;Keywords: hydrolase; metalloproteinase; zinc F;135-326/Domain: astacin homology <AST>
F;556-592/Domain: EGF homology <EG1>
F;596-705/Domain: EGF homology <EG2>
F;712-747/Domain: EGF homology <EG2>
F;218,222,228,277/Binding site: zinc (His, His, HF;219/Active site: Glu #status predicted
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F;860-973/Domain: Clr/Cls repeat homology <ClR4>
F;950-973/Domain: Clr/Cls repeat homology <ClR5>
F;91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted F;163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,6 F;213,211,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted F;214/Active site: Glu #status predicted F;5155,720/Modified site: arrhunther the contraction of t
                                                                C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-19 (.)Accession: T09456
R;Kozyraki, R.; Kris
Blood 91, 3593-3600,
A;Title: The human i
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A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: I49540; MUID:94229342; A;Accession: I49540
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Dev. Biol. 163, 175-183, 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     procollagen C-endopeptidase (EC 3.4.24.19)
C;Species: Mus musculus (house mouse)
C;Date: 02-Uul-1996 #sequence_revision 02-UC;Accession: I49540
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Best Local S
Matches 43
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;591-700/Domain:
;707-742/Domain:
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ilarity 39.4%;
Conservative 18
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C1r/C1s repeat hom
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Pred. No. 4.9e-06;
8; Mismatches 43
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Pred. No. 4.8e-06;
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A;Reference number: Z16677; MUID:98241400; PMID:9572993
A;Accession: T59456
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3623 <KOZ>
A;Cross-references: UNIPROT:060494; EMBL:AF034611; NID:93
C;Genetics:
A;Map position: 10p12
C;Superfanily: intrinsic factor-B12 receptor cubilin; EGF
C;Keywords: receptor; vitamin B12 uptake
F;1-24/Domain: signal sequence #status predicted <SIG>F;25-3623/Product: intrinsic factor-B12 receptor #status
F;436-467/Domain: EGF homology <BGF>
                                                                                                               A;Cross-references: GB:D10467; GB:D01077; NID:g222962; PIDN:BAA01260.1; PID:g222963
A;Experimental source: tadpole, brain
A;Note: this protein has motifs homologous to complement components C1r and C1s and to C;Comment: This protein is a neuronal cell surface molecule involved in the neuronal re C;Superfamily: Xenopus A5 antigen; C1r/C1s repeat homology; discoidin I amino-terminal C;Keywords: duplication; glycoprotein; transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>F;22-927/Product: A5 antigen #status predicted <A5A>F;22-138/Jomain: C1r/C1s repeat homology <C1R1>F;147-262/Jomain: C1r/C1s repeat homology <C1R2>F;274-424/Domain: discoidin I amino-terminal homology <DN1>F;370-584/Domain: discoidin I amino-terminal homology <DN1>F;370-584/Domain: discoidin I amino-terminal homology <DN2>F;370-584/Domain: discoidin I amino-termina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A5 antigen precursor - African clawed frog (Species: Xenopus laevis (African clawed frog) (C;Species: Xenopus laevis (African clawed frog) (C;Adte: I0-Sep-1999 #sequence_revision 10-Sep-1999 #text_change: C;Accession: JH0466; J0948 R;Takagi, S.; Hirata, T.; Agata, K.; Mochii, M.; Eguchi, G.; Fuj: Neuron 7, 295-307, 1991 A;Title: The Apartian a candidate for the neuronal recognition A;Reference number: JH0466; MUID:91337458; PMID:1908252 A;Accession: JH0466
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                                                                          :646-812/Domain: MAM homology <MAM>
:861-883/Domain: transmembrane #sta
  Query Match
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Pred. No. 4.4e-05;
4; Mismatches 120
     Score 176;
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Cell 67, 469-481, 1991
A;Title: The Drosophila dorsal-ventral patterning gene tolloid
A;Title: The Drosophila dorsal-ventral patterning gene tolloid
A:Dafarance number: A39288; MUID:92034970; PMID:1840509
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A; Residues: 1-1057 <SHI>
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                      64 VQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRYDFVEVEDISETS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         duplication; hydrolase; metalloproteinase;
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                         AKRYSCTPRNYSVNIREELKLANVVFFPRCLL---
                                                                                                                         DKKIAEFDTVEDLLKYFNPESWQEDLENMYLDTPRYRGRSYHDRKSKVD----LDRLNDD
                                                                                                                                                                                                                                                                       SRLIGRECGDK-LPPNIKTRSNOMYIREVSDS-SVOKLGESAALMLDVDECKETDHGCQH
                                                                                                                                                                                                                                                                                                                        TIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFK----
                                                                                                                                                                                                                                                                                                                                                                          IDSPNYPMDYMPDKECVWRITAPDNHQVALKFQS-FELE--KHDGCAYDFVEIRDGNHSD
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                                                                          NSKQCVWEVVA-----
                                                                                                                                                                          LCINTLGSYQCGCRAGYELQANGKTCEDACGGVVDATKSNGSLYSPSYPDVYP
                                                                                                                                                                                                                         IYYSLLEDFQPAAAS----ETNWESVTSSISGV-----
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Pred. No. 5.1e-05;
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5; Mismatches
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lloproteinase; zinc
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PID: 915730

rep

human

melanog

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RLKKIGIYCGHELPPVVNSEQSILRLEFYSDRTVQRSGFVAKFVIDVDECSM

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C;Superfamily: intrinsic factor-B12 receptor cubilin; C;Keywords: egg yolk; endocytosis; glycoprotein; intess F;1-20/Domain: signal sequence #status predicted <SIG-F;21-3623/product: intrinsic factor-B12 receptor CUBIL F;133-164/Domain: EGF homology <EGF1>F;436-467/Domain: EGF homology <EGF7>
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A;Residues: 1-3623 <MOE>
A;Cross-references: UNIPROT:070244; EMBL:AF022247; NID:g3834379; PIDN:AAC71661.1;
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J. Biol. Chem. 273, 5235-5242, 1998
A;Title: The intrinsic factor-vitamin B12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        intrinsic factor-B12 receptor CUBILIN precursor -
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999
C;Accession: T08618
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A; Map position: 11q23
C; Keywords: transmembrane
                                                                                            A;Cross-references: UNIPROT:Q9BY79; DDBJ:AB055505 C;Comment: This protein, which plays key roles in
                                                                                                                                                                                             A; Title: Molecular cloning and characterization of MFRP, A; Reference number: JC7629; MUID:21164708; PMID:11263980
                                                                                                                                                                                                                                                                         membrane-type frizzled-related protein - human C;Species: Homo sapiens (man) C;Date: 30-Jun-201 #sequence_revision 30-Jun-: C;Accession: JC7629
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                                                                              ubilin
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                                                                                                                                                      A; Molecule type: mRNA
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                                                                                                                                                                                                                  Biophys. Res. Commun. 282, 116-123, 2001 Molecular cloning and characterization of MFRP,
                                                                                                                                                                                                                                                                                                                                                                                                                                      1058
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26.4%;
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No. 0.00033;
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CUBILIN #status predicted
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stine; kidney;
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C;Species: Xonopus laevis (African clawed frog)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999
C;Accession: T30337
                                                                                                                                                                                         RESULT
S58984
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                                                                                                                       development protein tolkin (EC 3.4.24.
C;Species: Drosophila melanogaster
C;Date: 19-Jul-1996 #sequence_revision
C;Accession: $58984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-1524 <YAN>
A;Cross-references: UNIPROT:Q91674; EMBL:U81290; NID:g2981640; C;Superfamily: tryosin related polyprotein; trypsin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.
submitted to the EMBL Data Library, March 1998
A;Description: cDNA cloning of ovochymase, a chymotrypsin-like
A;Reference number: Z20829
A;Accession: T30337
             A; Molecule type: mRNA
A; Residues: 1-1464 < FIN>
                                            A;Title: The tolkin gene is A;Reference number: S58984; A;Accession: S58984
                                                                                           R; Finelli, A.L.; Xie, T.; B
Genetics 141, 271-281, 1995
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Pred. No. 0.0019;
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9; Mismatches
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Pred. No. 0.00024;
 EMBL: U34777;
                                                                                                                                           26-Jul-1996
                                                                                                           Blackman,
                                                           PMID:8536976
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   PIDN: AAC47015.1;
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trolloid-BMP-1 like protein 1 - California sea hare
N;Alternate names: probable metalloprotease TBL-1
C;Species: Aplysia california (California sea hare)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31069
R;Liu, Q.R.; Hattar, S.; Endo, S.; MacPhee, K.; Zhang, H.; Cleary, L.J.; Byrne, J.H.; Es
J. Neurosci. 17, 755-764, 1997
A;Title: A developmental gene (Tolloid/BMP-1) is regulated in Aplysia Neurons by treatme
A;Reference number: Z20965; NUID:98007484; PMID:8987797
A;Accession: T31069
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1070 <LIU>
A;Residues: 1-1070 <LIU>
A;Cross-references: UNIFROT: P91972; EMBL:U57369; NID:g1899041; PID:g1899042; PIDN:AAC474
C;Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; C1r/C1s repe
RESULT 17
A59271
Ra-reactive factor (EC 3.4.21.-) 2 precursor - human
Ra-reactive factor (EC 3.4.21.-) 2 precursor - human
N;Alternate names: mannose binding protein-associated serine proteinase 2 (NC;Species: Homo sapiens (man)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
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Genetics:
Gene: tolkin
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;S93-722/Domain: astacin homology cAST>

;958-993/Domain: EGF homology cEGF>

;1118-1153/Domain: EGF homology cEGF1>

;614,618,624,673/Binding site: zinc (His,

;615/Active site: Glu #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                           SGTISSPSFPDLYPPDKNCVWHISAPKGHTLTVNFTHMD--LEWRGDECELDFVRVTNVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GESESSSVLGRFCGDK-IPFPISSTSNOMYMVLKTDKN-KOKNGFTASHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 149; DB 2;
Pred. No. 0.0044;
4; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 153; DB 2;
Pred. No. 0.0033;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1070;
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A59386 sanko - human C;Species: Homo

sapiens

(man)

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R;Thiel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaeble, W.J.; Laursen, S.B.; Poulsen, Nature 386, 506-510, 1997
A;Title: A second serine protease associated with mannan-binding lectin that activates A;Reference number: A59271; MUID:97242412; PMID:9087411
A.Accession: A59271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 1p36.2-1p36.3

A;Map position: 1p36.2-1p36.3

C;Superfamily: complement-activating serine proteases Clr/Cls/MASP; Clr/Cls repeat homo C;Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-444,445-686/Product: Ra-reactive factor 2 #status predicted <MAT>
F;19-134/Domain: Clr/Cls repeat homology <CIR1>
F;142-180/Domain: Clr/Cls repeat homology <CIR2>
F;184-293/Domain: Clr/Cls repeat homology <CIR2>
F;184-293/Domain: Clr/Cls repeat homology <FH1>
F;300-361/Domain: complement factor H repeat homology <FH1>
F;345-6430/Domain: complement factor H repeat homology <FH2>
F;445-679/Domain: complement factor H repeat homology <FH2>
F;445-679/Domain: trypsin homology <TRY>
F;445-679/Domain: trypsin homology <TRY>
F;158/Modified site: sythro-beta-hydroxyasparagine (Asn) #status predicted
F;444-445/Cleavage site: Arg-Ile (autolytic) #status predicted
F;443-32,633/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: GDB: MASP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: parts of this sequence, including
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
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                                                                                                                                                                                                                                                                249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 ISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDD------------
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AOLAHA
                                                    RAKTMA
                                                                                                      GGQKAKPGDFPWQVLILGGTTAAGALLYDNWVLTAAHAVYEQKHDASALDIRMGTLKRLS
                                                                                                                                                                                                                                                              RSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQR-----
                                                                                                                                                                                                                                                                                                                                                                    YNSPSVTDPTLIADALDKKIAEF-----DTVEDLLKYFNPESWQEDLENMYLDTPRYRG
                                                                                                                                                                                                                                                                                                                                                                                                                        PPNGHVSPVQAKYILKDSFSIFCETGYELLQGHLPLKSFTAVCQKDGSWDRPMPACSIVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DREE----HGPFCG-KTLPHRIETKSNTVTITFVTDESGDHTGWK1HYTSTAHACPYPMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --YFVAKPGFKIY----YSLLE-----DFQPAAASETNWESVTSSISGVS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.4%;
18.8%;
                                                                                                                                                                                                               -- KVNDG--KYVCEADGFWTSSKGEKSLP-
                                                                                                                                                                                                                                                                                                                     DDLPSGRVEYITGPGVTTYKAVIQY----SCEETFYTM-----
                                                                                                                                                       CGGNCGCGTV---NWRSCTCNSGKTVKKYHEVLQFEPGHIKRRG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54;
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Pred. No. 0.0029;
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C;Date: 31-De
C;Accession:
R;sanko, S.
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I54763
A;Map position: 3q27-3q28
C;Superfamily: complement-activating serine proteases Clr/Cls/MASP; Clr/Cls repeat
C;Keywords: beta-hydroxyasparagine; complement pathway; duplication; glycoprotein;
F;1-17/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-234,'E',236-284,'G',286-498,'K',500-542,'K',544-642,'S',644-699
A;Cross-references: DDB:D17525; NID:g439712; PIDN:BAA04477.1; PID:g439713
A;Experimental source: liver
                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P48740; GB:D28593; NID:g790963; PII R;Takada, F.; Takayama, Y.; Hatsuse, H.; Kawakami, M. Biochem. Biophys. Res. Commun. 196, 1003-1009, 1993 A;Title: A new member of the C1s family of complement proteins A;Reference number: JN0883; MUID:94059062; PMID:8240317 A;Accession: JN0883
                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: I54763; JNO883
R;Sato, T.; Endo, Y.; Matsushita, M.; Fujita, T.
Int. Immunol. 6, 665-669, 1994
A;Title: Molecular characterization of a novel serine protease A;Reference number: I54763; MUID:94289349; PMID:8018603
A;Accession: I54763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ra-reactive factor (EC 3.4.21.-) 1 precursor - human N;Alternate names: mannose binding protein-associated serine pro C;Species: Homo sapiens (man) C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change
                                                                                         A;Gene: GDB:MASP1; GDB:CRARF; CRARF1; PRSS5; A;Cross-references: GDB:361104; GDB:330954;
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A; Molecule type: protein
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Best Local
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                                                                                                                                                      Comment: This is a serum bactericidal factor that
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sion: A59386
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Pred. No. 0.03;
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R;Wu, X.; Gattung, S. submitted to the EMBL Data Library, Januar A;Description: The sequence of C. elegans A;Reference number: 220722
A;Accession: T30018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;18-44B,449-699/Product: Ra-reactive factor #status pr;19-135/Domain: Clr/Cls repeat homology <ClR1>
F;14-135/Domain: EGF homology <EGF>
F;143-181/Domain: Clr/Cls repeat homology <ClR2>
F;185-294/Domain: Clr/Cls repeat homology <ClR2>
F;367-432/Domain: complement factor H repeat homology
F;367-432/Domain: complement factor H repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F38E9.2 - Caenorha
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision
C;Accession: T30018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;449-691/Domain: trypsin homology <TRY>
F;449-691/Domain: trypsin homology <TRY>
F;49,178,407/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;73-91,143-157,153-166,168-181,185-212,242-260,301-349,329-362,367-414,397-432,436-572,
F;159/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;448-449/Cleavage site: Arg-Ile (autolytic) #status predicted
F;490,552,646/Active site: His, Asp, Ser #status predicted
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                                       Вb
                                                                          δ
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A; Residues: 1-767 < W
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;Introns: 13/1; 37/3;
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    ETS----TIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLEDFQPA 176
                                           GVIHSPKYPESYPPNSDCQWTIHVDENSQVAIEF-VYFHLEQHKE--CIYDRLILTEGIS
                                                                              GYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRYD-FVEVEDIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMYLDTPRYRGRSYHDRKSKVDLD
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19.5%;
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Pred. No. 0.0071;
                                                                                                                                          Score 141.5; [Pred. No. 0.01;
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_			4.56EALLFT-TPRNRVRIEFSSDSSVERDGFFANFIADFDECQNDNAGCEHTCQN 506	261 DRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLL-VQRC-GGNCGCG 309	455	206 IADALDKKIAEFDTVEDLLKYFNPESWQEDLENMYLDTPRYRGRSYHDRKSKVDL 260	345 ATDKNICHHYCVNTVGGFKCACRVGYSLSSNGFSCDSTCGGYLKASNGSISSPNFPEMYP 404	205
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Q9UQ00
Q7LC53
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Q9WVM6
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Q8CG43
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Q95RA3
Q9JJS9
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O35375 mus musculu
O7gahl anopheles g
O8ifx2 crassostrea
O91674 xenopus lae
O8k480 mus musculu
O8cg43 rattus norv
O20176 caenorhabdi
O95ra3 drosophila
O9jjs9 rattus norv
O233995 drosophila
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Q8uvro gallus gall
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Q9qwj rattus norv
Q8uvqo gallus gallus
Q8fr18 ilyanassa o
Q8ff16 brachydanio
Q6g381 mus musculu
Q01654 halocynthia
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Octu67 brachydanio
Octu22 brachydanio
Octu70 brachydanio
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EMBL; AB03382; BAB18903.1; -.
EMBL; AF033824; AAK39287.1; -.
EMBL; AF335584; AAK39840.1; -.
EMBL; AF335584; AAK36136.1; -.
EMBL; AF336376; AAK20081.1; -.
EMBL; AY027517; AAK20081.1; -.
PIR; JC7591; JC7591.

HSSP; O9JUS8; INTO.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; F:growth factor activity; IE
GO; GO:0008151; P:cell growth and/or mainten
InterPro; IPR000072; PD_growth factor.
InterPro; IPR000072; PD_growth factor.
InterPro; IPR01916; TONB_Box_N.
Pfam; PF00431; CUB; 1.
SMART; SM00042; CUB; 1.
SMART; SM00141; PDGF; 1.
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01-MAR-2001
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LaRocchelle W.J., Jeffers M., McDonald W.F., Chillakuru R.A.,
Glese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet
Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets J.,
Shimkets R.A., Rothberg J.M., Lichenstein H.S.;
"PDGF D. A Novel Protease-Activated Growth Factor.";
Nat. Cell Biol. 3:517-521(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Xu Y.Y., Ye J., Song L., Gao Y., Zhang J., Wei Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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MEDLINB=21092670; PubMed=11162582; DOI=10.1006/bbrc.

Hamada T., Ui-Tei K., Imaki J., Miyata Y.;

"Molecular cloning of SCDGF-B, a novel growth factor

SCDGF/PDGF-C/fallotein.";
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01-MAR-2001 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Spinal cord-derived growth factor-B (MSTP036) (Platelet-derived growth factor D) (Iris-expressed growth factor long form).
Name=hSCDGF-B; Synonyms=IEGF, PDGFD;
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Alitalo K., Eriksson
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Mammalia; Eutheria;
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Uutela M., Li X., Pietras
Eriksson U.;
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Catarrhini;
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Best Local S
Matches 370
                   Hopkins R.F., Diatchenko L., P
WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R. L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler Altschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F. Diattchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheet Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange
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PROSITE;
PROSITE;
SEQUENCE
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
25-CCT-2004 (TrEMBLrel. 28, Last annotation update)
Iris-expressed growth factor short form (Platelet d factor D, isoform 2) (SCDGF-B).
Name=IEGF, Synonyms=PDGFD; ORFNames=UNQ1899;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                              "Expressed sequence tag analysis of adult human ir: Project: steroid-response factors and similarities pigment epithelium.";
                                                                                                                                                                                                                                                                                                                                                              Wistow G., Berstein S.L., Ray S., W Bouffard G., Smith D., Peterson K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9BWV5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAMB60
                                                                                                                                                                                                TISSUE=Testis
                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Iris;
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370; Conserv
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PS50278; I
PS00430; 7
370 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=12107412;
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PDGF_2; 1.
TONB_DEPENDENT_REC_1; UNKNOWN
TONB_DEPENDENT_REC_1; UNKNOWN
; 42848 MW; D387F485E7BB7674
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Primates;
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Pred. No. 7.7e-142;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                       Wyatt M.K.,
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1. CRC64;
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N.K.,
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Query Match
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Matches 364
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PIR; JC7591.

PIR; JC7591, 1WT0.

HSSP; Q3UJ88; 1WT0.

G0; G0:0016020; C:membrane; IEA.

G0; G0:0018083; F:growth factor activity; IEA.

G0; G0:0098151; P:cell growth and/or maintenance;

G0; G0:0098151; CUB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; pro0431; CUB; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS0278; PDGF 2; 1.
PROSITE; PS00430; TONB_DEPENDENT_REC 1; UNKNOWN_PROSITE; PS00430; TONB_DEPENDENT_REC 1; UNKNOWN_PROSITE; PS00430; AA; 42166 MW; 245C53E8DDEA9EAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-22887296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J. Chen J., Chow B., Chui C., Crowley C., Currell B., Dewel B., Dowd Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D. Yis., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bioinformatics assessment.", genome Res. 13:2265-2270(2003). Genome Res. 13:2265-2270(2003). EMBL; AV037518; AAAK20008-1; -. EMBL; BC030645; AAH30645.1; -. EMBL; AX355116; AAQ89474.1; -.
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LDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQ
                                                                                                       TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMY
                                                                                                                                                                                                          ETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLEDFQPAAASE
                                                                                                                                                                                                                                                                                                          NGYVQS PRF PNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRYDFVEVEDIS
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Matches
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MEDLINE=21092670; PubMed=11162582; DOI=10.1006/bbrc.2

Hamada T., Ui-Tei K., Imaki J., Miyata Y.;

Molecular cloning of SCOGF-B, a novel growth factor SCOGF/PDGF-C/fallorein.";

Biochem. Biophys. Res. Commun. 280:733-737(2001).

EMBL; ABB52170; BAB18920.1; -.

PIR; JC7592; JC7592.

HSSP; O90CV4; INZI.

GO; GO:0008083; F:growth factor activity; IEA.

GO; GO:0008151; P:cell growth and/or maintenance; IEA.
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01-OCT-2003
Spinal-cord
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Q9EQT1;
01-MAR-2001
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PROSITE; PS50278; PDGF 2;
SEQUENCE 370 AA; 4,2809
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SMART; SM00141; PDGF; 1
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Mammalia, Eutheria,
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RCGGNCGCGTLNWKSCTCSSGKTVKKYHEVLKFEPGHFKRRGKAKNMALVDIQLDHHERC
                     RCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC
                                                                                       MDTPRYRGRSYHERKSKVDLDRLNDDVKRYSCTPRNHSV
                                                                                                              LDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQ
                                                                                                                                                                                                       TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMY
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(TYEMBLrel. 16, Last sequence update)
(TYEMBLrel. 25, Last annotation update)
derived growth factor-B.
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Rodentia;
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Pred. No. 2.3e
23; Mismatches
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Sciurognathi;
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Yata Y.;
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RESULT
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Q92517; Q9D1LB;
Q92517; Q9D1LB;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
05-JUL-2004 (TrEMBLrel. 2
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Platelet-derived growth factor D (Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110003109 product:platelet-derived growth factor D).
Name=Pdgfd;
                                                                                                                                                                                                                                                                                                                             "Analysis of the mouse transcriptome based o 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
STRAIN=C57BL/6J; TISSUE=Whole body;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
                                                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE=Whole body;

MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs
prepare full-length cDNA libraries for rapid discovery of new
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE 2108566; PubMed=11217851; I
RIKEN FANTOM Consortium;
"Functional approximations"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21231380; PubMed=11331882; DOI=10.1038/35074593; LaRochelle W.J., Jeffers M., McDonald W.F., Chillakuru R Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang I Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets R.A., Rothberg J.M., Lichenstein H.S.; "PDGF D, A Novel Protease-Activated Growth Factor."; Nat. Cell Biol. 3:517-521(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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STRAIN=C57BL/6J; TISSUE=Whole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001).
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STRAIN=C57BL/6J; TISSUE=Whole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Whole body; MEDLINE=99279253; PubMed=10349636; l Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA c. Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Whole
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Q6V9H4

PRELIMINARY;

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Genome Res.
[7]
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GO; GO:0050730; P:regulation of
Pfam; PF00431; CUB; 1.
SMART; SM00042; CUB; 1.
SMART; SM00141; PDGF; 1.
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PROSITE; PS50278; PDGF 2; 1.
SEQUENCE 370 AA; 42809 MW;
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                                                          DCICSSRPPR
                                                                               RCGGNCGCGTVNWKSCTCSSGKTVKKYHEVLKFEPGHFKRRGKAKNMALVDIQLDHHERC
                                                                                          RCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC
                                                                                                                      LDTPHYRGRSYHDRKSKVDLDRLNDDVKRYSCTPRNHSVNLREELKLTNAVFFPRCLLVQ
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85.1%;
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Pred. No. 1
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peptidyl-tyrosine
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I., Sakai K.,
Shiraki T.,
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Best Local Sim
Matches 274;
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01-OCT-2002
01-OCT-2003
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Pdgfd protei
SEQUENCE FROM N.A.

STRAIN=FVB/N; TISSUE=Mammary tumor;

STRAIN=FVB/N; TISSUE=Mammary tumor;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12.1073/pnas.242603899;

MELANDER R. D., COLLING F. S., Schemmen C.M., Hong L.,

MALESCHUL S.F., Jordan H., Moore T., Max S.I., Wang J., Hish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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Submitted (JUL-2003) to the
EMBL; AY347260; AAQ24382.1;
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                      Pdgfd protein.
Name=Pdgfd;
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PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF_2;
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Pfam; PF00431; CUB; 1:
SMART; SM00042; CUB; 1
                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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GO; GO:0008083; F:growth factor activ
GO; GO:0008151; P:cell growth and/or
InterPro; IPR000859; CUB.
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Mammalia; |
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
utheria; Lagomorpha; Leporidae; Oryctolagus.
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Rodentia;
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91.3%;
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Last sequence
Last annotation
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; I
Sciurognathi; Muridae;
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id/or maintenance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence up
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Murinae; Mus
                                                                         Scheetz T.E.,
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"Generation and initial analysis of more than 15,000 full-len and mouse cDNA sequences.";

"Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                            Q91946;
01-OCT-2000 (TrEMBLrel. 15, 0
01-OCT-2000 (TrEMBLrel. 25, 1
01-OCT-2003 (TrEMBLrel. 25, 1
Spinal cord-derived growth fe
Name=SCDGF;
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Pfam; PF00431; CUB; 1.
SMART; SM00042; CUB; 1.
PROSITE; PS01180; CUB; 1.
SEQUENCE 261 AA; 30228 M
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Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                        Q91946
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MGI:1919035; Pdgfd.
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                                                                                                                                                                                                                                gallus (Chicken).
ota; Metazoa; Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLEDFQPAAASE
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Pred. No. 7.8e
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                             Craniata; Ver
; Galliformes;
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peptidyl-tyrosine
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                                                                                                                                                                                                                                                                                                                                                                                                                          345
                                                                                                                                                                                                             Vertebrata; Euteleostomi;
mes; Phasianidae; Phasiani
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A., Schein J.
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G.G.,
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STRAIN=white leghorn; TISSUE=Spinal MEDLINE=20317014; PubMed=10858496; Hamada T., Ui-Tei K., Miyata Y.; "A novel gene derived from developi member of the PDGF/VEGF family.";

developing

spinal

cords,

18

a unique

1 cord; DOI=10.

.1016/S0014-5793 (00) 01640-9;

SEQUENCE FROM N.A.

Aves;

Neognathae;

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RESULT
Q9QY71
ID Q9
AC Q9
AC Q9
AC Q9
AC B
DD T 01
DT 01
DT 01
DT 01
DE pr
DE pr
DE pr
DE pr
DE pr
DE DE Q1
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Best Local
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Q9QY71;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Fallotein (Platelet-derived growth factor C) (Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130403008
product:platelet-derived growth factor, C polypeptide, full insert sequence) (Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730022G11 product:platelet-derived growth factor, C polypeptide, full-length enriched library, clone:A73002G11 product:platelet-derived growth factor, C polypeptide, full-length enriched library, clone:D30001M08 product:platelet-derived growth factor, C
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GO; GG
GO; GG
   SEQUENCE FROM TISSUE=Ovary;
                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                         Mus
                                                                                                                                                                                                                                                       polypeptide, full insert sequence)
Name=Pdgfc;
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PROSITE; PS50278; PDGF 2; 1.
Growth factor; Mitogen.
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SMART; SM00141; PDGF; 1.
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InterPro; IPR000072; PD_growth_factor
Pfam; PF00431; CUB; 1.
Pfam; PF00341; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   musculus (Mouse)
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GO:0008033; P:growth factor activity;
GO:0008233; P:cell proliferation; IEA,
GO:0000074; Piregulation of cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEDPEDDICKYDFVEVEEPSDGTVL--GRWCGSSSVPSRQISKGNQIRIRFVSDEYFPSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                             Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38940 MW;
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Pred. No. 1.8e-48;
                                                                                                                                     Craniata; Vert
Sciurognathi;
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RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
C. -!- SIMILARITY: Belongs to the PDGF/VFGF/Trouth feature f.--*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TUSUE=Cccum, Cerebellum, and Head;

STRAIN=C57BL/6J; TUSUE=CCcum, Cerebellum, and Head;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

X Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

X Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Itch M.,

X Sumi N., Tahii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

X Sumi N., Tahii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

X Sumi N., Tahii Y., Nakamura S., Hazama M., Nishine T., Kashiwagi K.,

X A Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

X Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

X Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

X Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

X Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

Sequencing pipeline with 384 multicapillary sequencer.";

L. Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
STRAIN-C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs
prepare full-length cDNA libraries for rapid discovery of new
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tsai Y.-J.
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Cecum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based c 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Cecum,
The FANTOM Consortium,
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STRAIN=C57BL/6J; TISSUE=Cecum, Cere
MEDLINE=21085660; PubMed=11217851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gao Z., Hart C., Piddington C., Gilbertson D., West J., O'Hara Submitted (MAY-2000) to the EMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN
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STRAIN=C57BL/6J;
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STRAIN=C57BL/6J;
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SIMILARITY: Belongs to the L; AFI17608; AAF72516.1; -- L; AF266467; AAK58566.1; -- L; AK033734; BAC28455.1; -- L; AK042767; BAC31358.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FANTOM Consortium;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -K., Chen Y.-H., Lin S.-P., Cheng W. to the EMBL/GenBank/DDBJ databases.
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851; DOI=10.1038/35055500;
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536; DOI=10.1016/S0076-6879(99)03004-9;
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P.J.;
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annotation
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Best Local S
Matches 148
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InterPro; IPR000072; PD growth
Pfam; PP00431; CUB; 1.
Pfam; PP00341; PDGF; 1.
SMART; SM00042; CUB; 1.
SMART; SM00041; PDGF; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS0178; PDGF 2; 1.
Growth factor; Mitogen.
                                                                                                                                                                                                                                                                                                            Q8CI19 PRELIMINARY;
Q8CI19;
Q1-MAR-2003 (TrEMBLrel. 2
Q1-MAR-2003 (TrEMBLrel. 2
Q1-OCT-2003 (TrEMBLrel. 2
Platelet-derived growth f
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GO; GO;
GO; GO;
SEQUENCE FROM N.A.

STRAIN=CZECH II; TISSUE=Mammary tumor;

MEDLINE=22388257; bubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler (
Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.;

Altechul S.F., Zoeberg B., Buetow K.H., Schaefer C.F., Bhat N.;

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheet

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange

Branda S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah
                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
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GO:0005161; F:platelet-derived growth factor receptor bin.
GO:0008184; F:positive regulation of cell proliferation; IDA.
GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla.
GO:0007171; Ptransmembrane receptor protein tyrosine kin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGFKIYYSLLEDFQPAAASETNWESVTSSISGVSYNSPSVTDP-TLIADALDKKIAEFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - KTGVKGLHKSLTDVALEHHEECDCVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                       Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38741 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.7%;
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23, Last sequence update)
25, Last annotation update)
factor, C polypaptide.
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Pred. No. 2.1e
59; Mismatches
                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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1es 92;
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 Scheetz 1., Scheetz 1., Trange C.,
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                                       T.E.,
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       RESULT
Q9EQX6
ID Q9
AC Q9
DT 01
DT 01
DT 01
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Q9EQX6;
01-MAR-2001
01-MAR-2001
01-OCT-2003
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Query Match
Best Local S
Matches 147
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R MGD; MGI:1859631; Pdgfc.

R GO; GO:0005615; C:extracellular space; TAS.

R GO; GO:0005615; C:extracellular space; TAS.

R GO; GO:0005161; F:platelet-derived growth factor receptor bin...

R GO; GO:0005171; P:platelet-derived growth factor receptor bin...

R GO; GO:0000717; P:regulation of peptidy1-tyrosine phosphoryla...

R GO; GO:0000717; P:transmembrane receptor protein tyrosine kin...

R InterPro; IPR000859; CUB.

R InterPro; IPR000859; CUB.

R InterPro; IPR000872; PD growth factor.

R Pfam; PF00431; PUGF; 1.

R Pfam; PF00431; PDGF; 1.

R Pfam; PF00431; PDGF; 1.

R Pfam; PF001180; CUB; 1.

R PROSITE; PS01180; CUB; 1.

R PROSITE; PS01180; CUB; 1.

R PROSITE; PS01180; CUB; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the EMBL/GenBank/DDBJ databases.
EMBL; BC037696; AAH37696.1; -.
HSSP; Q9JJS8; INTO.
MGD; MGI:1859631; Pdgfc.
G0; G0:0005615.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE-Mammary
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314
                                   338
                                                                                                             278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
-KTGVKGLHKSLTDVALEHHEECDCVC
                                                                       VEDILKYFNPESWQEDLENMYLDTPRYRGRSY-HDRKSK-VDLDRLNDDAKRYSCTPRNY
                                                                                                                                                                                                                                                                PGFKIYYSLLEDFQPAAASETNWESVTSSISGVSYNSPSVTDP-TLIADALDKKIAEFDT
                                                                                                                                                                                                                                                                                                      LEDPEDDLCKYDFVEVEEPSDGSVL--GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSE
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                                                                                                                                                                                                                                                                                                                                                                                IKRRGRAKTMALVDIQLDHHERCDCIC
                                                                                                                                                                                                                            PGFCIHYSII---MPQVTETT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38741 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 750; DB
Pred. No. 3e-4
50; Mismatches
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tyrosinė kin. .
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A., Schein J.
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G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bin.
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(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.

16, 25,

Created) Last seq Last ann

annotation

update)

PRELIMINARY;

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Q9UL22
ID Q9UL2
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Best Local (
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                                                                                                                                      Q9UL22;
Q9UL22;
01-MAY-2000
                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Secretory growth factor-like protein fallotein (Spi:
growth factor) (Platelet-derived growth factor C) (
Name-hSCDGF; Synonyms-PDGFC; ORFNames-UNQ174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPRO00859; CUB.
InterPro; IPRO00072; PD_growth_factor.
Pfam; PF000431; CUB; 1.
Pfam; PF00341; PDGF; 1.
SMART; SM00042; CUB; 1.
SMART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP;
GO; GC
GO; GC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Wistar; TISSUE=Kidney;
MEDLINE=21092670; PubMed=11162582; DOI=
Hamada T., Ui-Tei K., Imaki J., Miyata
"Molecular cloning of SCDGF-B, a novel
SCDGF/DDGF-C/fallotein.";
Biochem. Biophys. Res. Commun. 280:733-
-!- SIMILARITY: Belongs to the PDGF/VEC
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01180; CUB; 1. PROSITE; PS50278; PDGF_2; 1.
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GO:0008083; F:growth factor activity;
GO:0008283; P:cell proliferation; IEA.
GO:000074; P:regulation of cell cycle
                        sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                           256
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Metazoa;
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Rodentia;
Chordata;
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Pred. No. 8.
Craniata;
                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280:733-737(2001)
PDGF/VEGF growth
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Vertebrata;
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                                                                    (Spinal C) (VEGE
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Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dow Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J. Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura Yis., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Uterus; PubMed=11004490; DOI=10.1016/S0167-4781(00)00066-X; Tsai Y.J., Lee R.K., Lin S.P., Chen Y.H.; "Identification of a novel platelet-derived growth factor-like gene, fallotein, in the human reproductive tract.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21347863; PubMed=11297552; DOI=10.1074/jbc.M3 Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., St Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.; "Platelet-derived growth factor C (PDGF-C), a novel cbinds to PDGF alpha and beta receptor."; Biol. Chem. 276:27406-27414(2001).
                                                                                                                                                                                                                                                                                                                                        EMBL; AY358493; AAQ88857.1; -.
HSSP; Q9JJS8; INTO.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0008083; F:growth factor activity;
GO; GO:0007417; P:central nervous system of
                                                                                                                                                                                                                                                                                                                                                                                                                bioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
EMBL; AF091434; AAF00049-1; -.
EMBL; AB033831; BAB03266.1; -.
EMBL; AF260738; AAK51637.1; -.
                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                              Pfam; PF00431; CUB; 1.
Pfam; PF00341; PDGF; 1.
PROSITE; PS01180; CUB;
PROSITE; PS50278; PDGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               effort to identify novel human
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Hamada T., Ui-Tei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Godowski P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The secreted protein discovery initiative
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                                                                                                                                                                                                                                                                                                      InterPro; IPR000859; CUB.
                                                                                                                                                                     159;
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                                                                                                                                                                                     Similarity
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              TIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSL-LEDFQPAAASETN
                                                                     QSPRFPNSYPRNLLLTWRLHS-QENTRIQLVFDNQFGLEEAENDICRYDFVEVEDISETS
                                                                                                                                     IFVYTLICANFCSCRDTSATPOSASIKALRNANLRRDESNHLTDLYRRDETIOVKGNGYV
                                             HSPREPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGT
                                                                                                          LFGLLLLTSALAGQRQGTQAESNLSSKFQFSSN---KEQNGVQD-PQHERIITVSTNGSI
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                                                                                                                                                                                                                                  345 AA;
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                                                                                                                                                                                                                                 ; CUB; 1.
; PDGF 2; 1.
A; 39029 MW;
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K., Miyata Y.;
                                                                                                                                                                                37.2%;
                                                                                                                                                                     59;
Score 742.5; vs.,
Pred. No. 1.1e-47;
9; Mismatches 114;
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                                                                                                                                                                                                                                  CDE9E51F40633E78 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOI=10.1016/S0014-5793(00)01640-9;
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                                                                                                                                                                                                                                                                                                                                           development;
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Sheppard P.
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STRAIN-Swise Webster/NIH;
MEDLINE-20417814; PubMed=10960785; DOI=10.1016/S0925-4773(00)00425-1;
MEDLINE-20417814; PubMed=10960785; DOI=10.1016/S0925-4773(00)00425-1;
Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
"The mouse pdgfc gene: dynamic expression in embryonic tissues during
                                                                                                                                                                                                                                                                                                                  PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF_2;
SEQUENCE 345 AA; 38886
                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00431; CUB; 1.
SMART; SM00042; CUB; 1.
SMART; SM00141; PDGF; 1.
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Mammalia; Eutheria;
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01-OCT-2000
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(MGI:1859631; Pdgfc.
GO:0005615; C:extracellular space; TAS.
GO:0005615; C:extracellular space; TAS.
GO:0005161; F:platelet-derived growth factor receptor bin.
GO:0005161; F:positive regulation of cell proliferation; IDA.
GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla.
GO:0007111; P:transmembrane receptor protein tyrosine kin.
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                                                                                                                                                                                        ESNHLTDLYRRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHS-QENTRIQLVFDNQFG
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                                                       PGFKIYYSLLEDPQPAAASETNWESVTSSISGVSYNSPSVTDP-TLIADALDKKIAEFDT
                                                                                                                                                                   EQNGVQD-PRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRTQLTFDERFG
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                   PGFCIHYSII---MPQVTETT
                                                                                            CEDPEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence
(TrEMBLrel. 25, Last annotation)
rived growth factor C.
                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Rodentia;
                                                                                                                                                                                                                                                             37.2%;
45.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                         PD_growth_factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYR
                                                                                                                                                                                                                                                                                                                    MW ;
                                                                                                                                                                                                                                             59;
                                                                                                                                                                                                                                                           Score 742; DB 2;
Pred. No. 1.2e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                      FA1486BED6D362F8 CRC64;
                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                             93;
                   SPSVLPPSSLSLDLLNNAVTAFST
                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                           Gaps
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                   195
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В
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9NRA1;
Q9NRA1;
01-OCT-2000 (
01-OCT-2000 (
01-OCT-2003 (
                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF_2;
Growth factor; Mitogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00431; CUB; 1.
Pfam; PF00341; PDGF; 1.
SMART; SM00042; CUB; 1.
SMART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew, HGNC:8801, PDGFC.
GO; GO:001.6020, C:membrane; IEA.
GO; GO:0008083, F:growth factor activity;
GO; GO:0008283, F:cell proliferation, IEA.
GO; GO:0000274, P:regulation of cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20268201; PubMed=10806482; DOI=10.1038/35010579; Li X., Ponten A., Aase K., Karlsson L., Abramsson A., Uu Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano F Betsholtz C., Heldin C.-H., Alitalo K., Ostman A., Eriks "PDGF-C is a new protease-activated ligand for the PDGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TYEMBLrel. 15, Created)
01-OCT-2000 (TYEMBLrel. 15, Last sequence update)
01-OCT-2003 (TYEMBLrel. 25, Last annotation update)
Platelet_derived growth factor C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF244813; AAR
HSSP; Q9JJS8; 1NTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000859;
InterPro; IPR000072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nat. Cell Biol. 2:302-309(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                    y Match
Local (
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 172
                                                                                                                                                                                                                                                                                                   159;
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                                   183
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                                                                                                                                                                                                                                                                                                                    Similarity
                                                                      --ILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAV----
                                                                                          TIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSL-LEDFQPAAASETN
                                                                                                                                             HSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGT
                                                                                                                                                                       QSPRFPNSYPRNLLLTWRLHS-QENTRIQLVFDNQFGLEEAENDICRYDFVEVEDISETS
                                                                                                                                                                                                                        FGLLLVTSALAGQRRGTQAESNLSSKFQFSSN---KEQNGVQD-PQHERIITVSTNGSI
                                                                                                                                                                                                                                                             I FVYTLI CANFCSCRDTSATPQSASI KALRNANLRDESNHLTDLYRRDETIQVKGNGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IKRRGRAKTMALVDIQLDHHERCDCIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVSIREELKRIDIRFWPGCLLVKRCGGNCACCLHNCNECQCVPRKVTKKYHEVLQLRP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSGKTVKKYHBVLQFEPGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYVKKSKVVNLNLLKEEVKLYSCTPRNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEDILKYFNPESMQEDLENMYLDTPRYRGRSY-HDRKSK-VDLDRLNDDAKRYSCTPRNY
                                 WESVISSISGVSYNSPSVIDPI-LIADALDKKIAEFDIVEDLLKYFNPESWQEDLENMYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -KTGVKGLHKSLTDVALEHHEECDCVC
                                                                                                                                                                                                                                                                                                                                                                               345
                                                                                                                                                                                                                                                                                                 37.2%; ilarity 43.6%; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                             A,
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Primates;
                                                                                                                                                                                                                                                                                                                                                                             39043 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUB.
   SPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERWOLDLEDLYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _growth_factor
                                                                                                                                                                                                                                                                                                     59;
                                                                                                                                                                                                                                                                                               Pred. No. 1.3e
); Mismatches
                                                                                                                                                                                                                                                                                                                                        Score
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Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                             590889CEASSCCSEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDGF/VEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell cycle;
                                                                                                                                                                                                                                                                                                                                        741.5;
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i; Hominidae;
                                                                                                                                                                                                                                                                                                                      .3e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ጅ
                                                                                                                                                                                                                                                                                                                                        DB
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PDGF alph
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BMP1_XENLA
                  RESULT 15
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0008083; F:ggrowth factor activity; IEA.
GO; GO:0008151; P:cell growth and/or maintenance; IEA
InterPro; IPR000859; CUB.
InterPro; IPR000072; PD_growth_factor.
InterPro; IPR000072; PD_growth_factor.
Pfam; PF00431; CUB; 1.
Pfam; PF00431; CUB; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01180; CUB; 1.
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                    Matches
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Q8K429;
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Sprague-Dawley; TISSUE=Skin; Brown S.A., Coberly D.M., Rohrich R.R., Chao J Submitted (MAY-2002) to the EMBL/GenBank/DDBJ EMBL; AF508348; AAM47265.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
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                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                               LANVVFFPRCLLVQRCGGNCGCGTVNWRSCTC 318
                                                                                                                                                                                                                                                  RRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHS-QENTRIQLVFDNQFGLEEAENDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTPRYRGRSY-HDRKSK-VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLV
                                                            RTDTIFWPGCLLVKRCGGNCACCLHNCNECQC 255
                                                                                                                   PDRWQIDLDSLYKPTWPLLGKAFLYGKKSKAVNLNLLKEEVKLYSCTPRNFSVSIREELK
                                                                                                                                  PESWQEDLENMYLDTPRYRGRSY-HDRKSK-VDLDRLNDDAKRYSCTPRNYSVNIREELK
                                                                                                                                                                             I---MPQVTETT
                                                                                                                                                                                                     LEDFQPAAASETNWESVTSSISGVSYNSPSVTDPTLIA-DALDKKIAEFDTVEDLLKYFN
                                                                                                                                                                                                                                    KYDFVEVEEPSDGSVL-
                                                                                                                                                                                                                                                                                          RHERVVTISGNGSIHSPKFPHTYPRNTVLVWRLVAVDENVRIQLTFDERFGLEDPEDDLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDCVC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDCIC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRCGGNCACCLHNCNECOCVPSKVTKKYHEVLQLRP---KTGVRGLHKSLTDVALEHHEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTWOLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLV
                                                                                                                                                                                                                                                                                                                                                                                                          258
258 AA;
                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                31.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                          258
                                                                                                                                                                                                                                                                                                                                                                                                           29255 MW; 88625B989FCC3F8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                  54;
                                                                                                                                                                                                                                   -GRWCGSGTVPGKQTSKGNHÍRÍRFVSDEYFPSEPGFCÍHÝSI
                                                                                                                                                                                                                                                                                                                                               Score 632; DB 2; 2. Pred. No. 1.6e-39;
                                                                                                                                                                             SPSVLPPSALSLDLLNNAVTAFSTVEELIRFLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               databases
                                                                                                                                                                                                                                                                                                                                                                             Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IEA.
                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                           163
                                                                                                                                                                                                      228
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                                                                                                                                                286
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      InterPro; IPRO00742; EGF 2.
InterPro; IPRO01881; EGF Ca.
InterPro; IPRO018029; EGF 1ke.
InterPro; IPRO06229; EGF M Zn BS.
InterPro; IPRO0625; Pept M Zn BS.
InterPro; IPRO01506; Pept MZn BS.
Pfam; PF00431; CUB; 3.
Pfam; PF00480; ASTACIN.
PROSITE; PS001010; ASTACIN.
PROSITE; PS001010; ASTACIN.
PROSITE; PS01180; CUB; 3.
PROSITE; PS01180; EGF 1; FALSE_NEG.
PROSITE; PS01187; EGF CA; 1.
                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR000859; CUB.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF_1ke.
InterPro; IPR006205; Pept_M_Zn_BS.
InterPro; IPR001506; PeptIdase_M12A.
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MEDLINE=94085787; PubMed=8262384; DOI=10.1016/0378-1119(93)
Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.;
"Cloning and expression of cDNA encoding Xenopus laevis bon morphogenetic protein-1 during early embryonic development.
Gene 134:257-261(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 45, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
Bone morphogenetic protein 1 precursor (EC 3.4.24.-) (BMP-1).
Benopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleost.
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; JC2218; , HSSP; P01130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                      Hydrolase; Metalloprotease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L12249; AAA16313.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -I- FUNCTION: Involved in pattern formation in gastrula and ladifferentiation of developing organs.

differentiation of developing organs.

-I- DEVELOPMENTAL STAGE: Blastula, early gastrula and hatched tadpoles; little or no expression in morula and late gastrulation of the peptidase M12A family.

-I- SIMILARITY: Contains 3 CUB domains.

-I- SIMILARITY: Contains 1 EGF-like domain.
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P98070;
   DISULFIL
                                                                                                                                                                                                                       Calcium;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                     PS00142; ZINC PROTEASE; 1. Chondrogenesis; Cytokine; EGF-like
    180
186
146
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   83
707
284
397
509
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176
177
180
186
Zinc (catalytic)
By similarity.
Zinc (catalytic)
Zinc (catalytic)
By similarity.
                                                                                                                                                                                                      Osteogenesis;
                                                                                       Metalloprotease.
CUB 1.
CUB 2.
EGF-like, calcium
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EMBL; D83476; BAA11922.1; -.
HSSP; B01130; 1HZB.
GO; GO:0008533; F:astacin activity; IEA.
GO; GO:0008537; F:astacin ion binding; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0006509; F:metallopeptidase activity; IEA.
GO; GO:0006509; P:protecolysis and peptidolysis; IEA.
GO; GO:0006509; P:protecolysis and peptidolysis; IEA.
Pfam; PF01400; Astacin; 1.
Pfam; PF00431; CUB; 5.
Pfam; PF00408; EGF; A; 1.
Pfam; PF07645; EGF CA; 1.
PRINTS; PR00400; ASTACIN.
                                                                                                             SMART; SM00042; CUB; 5.

SMART; SM00179; EGF CA; 2.

SMART; SM00215; ZMGC; 1.

PROSITE; PS0010; ASX HYDROXYL; 2.

PROSITE; PS01180; CUB; 5.

PROSITE; PS01186; EGF 2; 2.

PROSITE; PS01187; EGF 3; 2.

PROSITE; PS01187; EGF CA; 2.

PROSITE; PS01187; EGF CA; 2.

PROSITE; PS01142; ZINC PROTEASE; UNKNOWN 1.
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01-NOV-1996 (TREMBLIZE1. 0
01-NOV-1996 (TREMBLIZE1. 0
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Xenopus laevis (African clawed
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  ISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFK 164
                    KLNGSINSPGWPKEYPPNKNCIWQLVAPTQYRISLKFD
                                      KGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRYDFVEVED
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N-linked (GlCNAc. .) (Pot.
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EMBL/GenBank/DDBJ
                                                        Score 189.5; DB 2;
Pred. No. 1.8e-05;
8; Mismatches 38;
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Craniata, Vertebrata, Buteleostomi,
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SEQUENCE
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01-JUN-1998
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R GO; GO:0008533; F:astacin activity; IEA.
R GO; GO:0008533; F:astacin activity; IEA.
R GO; GO:0008539; F:calcium ion binding; IEA.
R GO; GO:0008539; F:calcium ion binding; IEA.
R GO; GO:0008509; F:calcium ion binding; IEA.
R GO; GO:0008508; P:proteolysis and peptidolysis; IEA.
R InterPro; IPR000152; Asx_hydroxyl_S.
R InterPro; IPR000859; CUB.
R InterPro; IPR000859; CUB.
R InterPro; IPR000859; CUB.
R InterPro; IPR000859; EGF_Ca.
DR InterPro; IPR006026; Peptidase_M.
InterPro; IP
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Pfam; PF07645; EGF CA; 1.

PRINTS; PR00408; ASTACIN.

SMART; SM00042; CUB; 3.

SMART; SM000179; EGF CA; 1.

SMART; SM00235; ZNMG; 1.

PROSITE; PS01180; CUB; 3.

PROSITE; PS01180; CUB; 3.

PROSITE; PS01186; EGF 3; 1.

PROSITE; PS051187; EGF CA; 1.

PROSITE; PS01187; EGF CA; 1.
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Dev. Biol. 194:144-157(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata;
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genetic protein 1b.
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Pred. No. 1.5e-05;
B; Mismatches 38;
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RX PubMed=1247793; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RX Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RX Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RX Altschal S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RX Hopkins R.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RX Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunarathe P.H.,
RX Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RX Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RX Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RX Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RX A Halten M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RX A Holting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RX A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RX A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RX A Topes S. J. Maxra M.A.
Query Match
                                                                                                                                                                                                                                                                                                                  InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR000529; CUB.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF_like.
InterPro; IPR006209; EGF_like.
InterPro; IPR006026; Peptidase_M.
                                                                                                                                                 Pfam; PF07645; EGF CA; 1.
PRINTS; PR00480; ASTACIN.
SMART; SM00042; CUB; 3.
SMART; SM00181; EGF; 1.
SMART; SM00179; EGF CA; 1.
SMART; SM00235; ZnMC; 1.
                                                     PROSITE;
PROSITE;
PROSITE;
                                                                                                             PROSITE;
                                                                                                                                                                                                                                            Pfam; PF01400; Astacin; Pfam; PF00431; CUB; 3. Pfam; PF00008; EGF; 1. Pfam; PF07645; EGF CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klein S., Gerhard D.S.; Submitted (AUG-2004) to the EMBL; BC080382; AAH80382.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones S.J., Marra M.A.; "Generation and initial analysis of and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopodinae;
NCBI_TaxID=8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BMP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2004 (TrEMBLrel. 25-OCT-2004 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Embryo;
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                                                   2; PS00010; ASX HYDROXYL; 1
3; PS01180; CUB; 3.
8; PS01180; EGF 2; 1.
2; PS01187; EGF CA; 1.
2; PS00142; ZINC_PROTEASE;
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                                     735
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                                     ΑĄ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sci.
                                 83603 MW;
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9.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U.S.A. 99:16899-16903(2002)
                                                       PROTEASE; UNKNOWN
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Last
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 Score 188.5;
                                     3D24DF86A4FAEBE4 CRC64;
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DB 2;
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Length 735;
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RESULT 19
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R GO; GO:0008509; F:calcium ion binding; IEA.
R GO; GO:0008237; F:metallopeptidase activity; IEA.
R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R InterPro; IPR00052; Asx_hydroxy1_S.
R InterPro; IPR000859; CUB.
NR InterPro; IPR000859; CUB.
NR InterPro; IPR000742; EGF_Ca.
NR InterPro; IPR000742; EGF_Ca.
NR InterPro; IPR006026; Peptidase_M.
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Matches 4
                                                                                             Query Match
Best Local (
                                                                                  Matches
                                                                                                                                                                                                                                                                                         Pfam; PF01400; Astacin; 1.
Pfam; PF00431; CUB; 5.
Pfam; PF000008; EGF; 1.
Pfam; PF07645; EGF CA; 1.
PRINTS; PR00480; ASTACIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8JI28;
Q8JI28;
01-OCT-2002
01-OCT-2002
                                                                                                                                                     PROSITE;
PROSITE;
PROSITE;
EGF-like
                                                                                                                                                                                                                                                     SMART; SM00042; CUB; 5.
SMART; SM00179; EGF_CA; 2.
SMART; SM00235; ZnMC; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                  PROSITE; PS00010; ASX HYDROXYL;
PROSITE; PS01180; CUB; 5.
PROSITE; PS01186; EGF 2; 2.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS01187; EGF CA; 2.
PROSITE; PS00142; ZINC_PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mech. Dev. 119:177-190(2002)
EMBL; AF393242; AAM73675.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expressed during early Xenopus development."; Mech. Dev. 119:177-190(2002). EMBL; AF393242; AAM73675.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=22352451; PubMed=12464431; DOI=10.1016/S0925-4773(02)00359-3;
Dale L., Evans W., Goodman S.A.;

"Xolloid-related: A novel BMP1/Tolloid-related metalloprotease
                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001506; Peptidase
InterPro; IPR006025; Pept_M_Zn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; M12.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xolloid-like metalloprotease.
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                                                      13
 64
                                                                                81;
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45; Conservative
                                                                                               Similarity
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1007 AA; 114364 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRYDFVEVED
VQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRYDFVEVEDISETS
                           ANFLKEEDECARPDNGGCEORCVNTLGSYKCSCDPGYELAPDKKSCEAACGGLLTKLNGT
                                                      ANFCSCRDTSATPQSAS----IKALRNANLRRDESNHLTDLYRRDET----IQVKGNGY
                                                                                   Conservative
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                                                                                               9.5%;
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                                                                                                                                                                    PROTEASE; UNKNOWN_1.
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26,
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Last
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8; Mismatches
                                                                                            Score 188.5; DB 2, Pred. No. 2.2e-05;
                                                                                   Pred. No. 2.26
1; Mismatches
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                                                                                                                                          3F33C686A7EF230C
                                                                                                                                                       Protease.
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ches 38;
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                                                                                   Indels
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                                                                                                                                                Query Match
Best Local Similarity
Matches 43; Conserv
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Pfam; PF07645; EGF CA; 1.

SMART; SM00042; CUB; 2.

SMART; SM00179; EGF CA; 1.

PROSITE; PS00101; ASX_HYDROXYL; 1.

PROSITE; PS01180; CUB; 2.

PROSITE; PS01186; EGF 2; 1.

PROSITE; PS01187; EGF CA; 1.
                                                                                                                                             Collagen;
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                     Hirahara I., Tomita M., Umeyama K., Urakami K.;

"New splicing pattern of the gene for procollagen c-proteinase.";

Cell Struct. Funct. 23:125-125(1998).

EMBL; AB012139; BAA75639.1; -.

HSSP; P00736; 1APQ.

MEROPS; M12.005; -.

GG; GO:0005599; F:calcium ion binding; IEA.

InterPro; IPR000152; ABX. hydroxyl_S.

InterPro; IPR000152; ABX. hydroxyl_S.

InterPro; IPR0001851; EGF_Ca.

InterPro; IPR001891; EGF_Ca.

InterPro; IPR001891; EGF_Ca.

InterPro; IPR001891; EGF_Like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Procollagen C-proteinase 3 (Fragment).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9Z135
Q9Z135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        751 CR-NGFVLHDNK------HDCKEAECEHRIHSSN------GVITSP------
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1.19 ISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYY 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     819 HQEC 822
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                             KLNGSITSPGWPKEYPPNKNCIWQLVAPTQYRISLQFD---FFETEGNDVCKYDFVEVRS 169
                                                       KGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRYDFVEVED 118
                                                                                                                                                                             EGF-like domain.
                                                                                                                                                241 AA; 27199 MW; 380803EBDE814EFA CRC64;
                                                                                   9.4%; Score 187.5; DB 2; Length ilarity 39.4%; Pred. No. 4.2e-06; Conservative 18; Mismatches 43; Indels
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                                                                                      43; Indels
                                                                                                                  241;
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170 GLTADSKLHGKFCG-SEKPEVITSQYNNNRVEFKSDN-TVSKKGFKAHF 216

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Search completed: November 10, 2005, 09:35:14 Job time: 170.998 secs

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1 MHRLIFVYTLICAL
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Aay96864 SEQ. ID.
Aab48653 Human gro
Aay71130 Human Pla
Aab60888 Human Pla
Aab60888 Human Pla
Aau000698 Human Zve
Aae00699 Human zve
Aae055601 Human ECT
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Aae15819 Human IP8
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1, porcine seminal plasma protein, bovine acidic seminal fluid protein cand Xenopus laevis tolloid-like protein. Structural analysis and homology predict that ZVEGF3 polypeptides complex with a second polypeptide to form multimeric proteins. The human zvegf3 gene has been mapped to chromosome 4q28.3. ZVEGF3 is useful for stimulating the growth of CC fibroblasts or smooth muscles cells, for activating cell surface PDGF-calpha receptor and for inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is useful for regulating (post-development) organ growth, regeneration and maintenance, as well as tissue maintenance and crepair processes. ZVEGF3 analysomator, is chemic limb disease, rheumatoid arthritis, diabetic retinopathy, ischemic limb disease, poripheral vascular disease, myocardial ischemia, vascular intimal hemmangioma formation. ZVEGF3 can also be used to modulate neurite growth can development of the nervous system, and for treating neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-DEC-1998;
06-JUL-1999;
21-OCT-1999;
12-NOV-1999;
                                                                                                                                                                                                                                                                                             (vascular endothelial growth factor homologue) are claimed. The growth factors comprise a growth factor domain and a CUB domain (generic sequence motifs are shown in AAY96859 and AAY96860). The growth factor domain is characterized by an arrangement of cysteine residues and beta strands that is characteristic of the "cysteine knot" structure of the platet-derived growth factor (PDGF) family. The CUB domain shows homology to CUB domains in neuropin homology to CUB domain shows
                                                                                                                                                                                                                                                                                                                                                                                                                       Polypeptides comprising an epitope-bearing portion human or murine ZVEGF3 (vascular endothelial growth factor homologue) are claimed. The growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 164-165; 173pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel zvegf3 polypeptides and nucleotides encoding them useful stimulating growth of smooth muscle cells and fibroblasts comparent bearing portion of a specific amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; zvegf4; growth factor homologue; VEGF/PDGF family; C PDGF-like activity; mitogenic; osteogenic; neovascularisati tissue repair; proliferation; differentiation; liver damage neuroregenerative; Alzheimer's disease; multiple sclerosis;
                          N-PSDB;
                                             WPI; 2000-687541/67
                                                                                  Gilbert
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10-NOV-1999;
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                                                                                  Hart CE,
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99US-0164463P.
2000US-0180169P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor homologue zvegf4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                                                                                                                                                                                                                                       hepatic;
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                                                                                                                                                                                                                                                                                                                                                                                                       bone fracture; wound healing; vulnerary; patic; chromosome 11q22.3-23.1.
                                                                                Sheppard
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Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   osteogenic; neovascularisation;
                                                                                  Gilbertson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC characterised by a POGF cystine knot structure, and a CUB domain CC (AAB8655) which has a beta barrel structure, and a CUB domain CC (AAB8655) which has a beta barrel structure, and a CUB domain CC muscle cells and pericytes, and has also been shown to stimulate bone growth. The invention also relates to fusion proteins comprising human comprising human zvegf4 or fragments thereof, particularly human zvegf4/human zvegf3 CC fusions; expression constructs and host cells comprising human zvegf4 conclete acids; the recombinant expression of human zvegf4, an antibody CC which binds to human zvegf4 or a fragment thereof; a method of activating a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a method of bone cells, comprising exposing bone cells to zvegf4-derived comprising exposing agenetic abnormality in the creatment of a patient. Zvegf4 proteins and derived fragments may be used to stimulate tissue development or repair, or cellular comprising exposing and may also be used to modulate or repair of liver damage, and may also be used to modulate or the treatment of periodontal disease and fractures. They may be used in the creatment of periodontal disease and fractures them cells and cells and condothelial precursor stem cells, which may be useful in the treatment of schemal, in wound healing, and in the modulation of the immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Sim.
Matches 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e.g. for tr
Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to the human growth factor homologue zvegf4 (AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial growth factor) family. Zvegf4 has a growth factor domain (AAB48654)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence
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                                                                                                                                                                                          DCICSSRPPR
                                                                                                                                                                                                                                                                                         RCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC
                                                                                                                                                                                                                                                                                                                                                                                               LDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMY
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                                                                                                                                                                                                                                                                                                                                                                  LDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQ
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Pred. No. 0;
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AAY71130 standard; protein; 370

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Query Match
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                                                                                                                   The present sequence is the complete human platelet derived growth factor (PDGF)-D, formally known as Vascular Endothelial Growth Factor (VEGF)-G. It is derived from human foetal lung lambdagt10 cDNA library. It belongs to the VEGF/PDGF family. It functions as an activator of proliferation, differentiation, growth and motility of cells, that express PDGF-D receptor. This sequence is useful for inhibiting the growth of tumours, that express PDGF-D. Expression of PDGF-D and its procepytic cleavage for generating an activated truncated form is useful for regulating receptor binding specificity of PDGF-D. PDGF-D antagonist is useful for inhibiting tissue remodelling during the invasion of tumour cells into normal cells. PDGF-D may be used to treat wounds, atherosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polynucleotides encoding a novel growth factor of a platelet-derived growth factor, useful for diagnostic applications, e.g. concerning cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnerary; VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour proliferative; activator; proliferation; differentiation; motility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-AUG-1999;
04-OCT-1999;
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28-DEC-1998;
                                                                                Sequence 370
                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; Fig 8; 111pp; English.
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nes 370; Conser
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99US-0150604P.
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Score 370; D
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The present invention relates to a vascular endothelial growth factor (VEGF) family member, VEGF-G. VEGF-G protein and nucleic acid molecules are used as modulating agents or as targets for developing modulating agents to regulate a variety of cellular processes e.g. cell proliferation, differentiation, migration and wound repair. VEGF-G modulators, i.e. VEGF-G protein, peptide, peptidomimetic or nucleic acid are used to treat a subject with aberrant VEGF-G protein or nucleic acid expression or activity e.g. deregulated cell growth, such as cancer, hyperptrophic bone disorders, disorders involving aberrant angiogenesis e.g. psoriasis, and chronic inflammatory diseases e.g. rheumatoid arthritis. VEGF-G gene expression is inhibited through the administration of antisense molecules or ribozymes and by targeting the regulatory region of VEGF-G to prevent transcription of the gene in target cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gearing
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Best Local
                     10-MAR-2000;
08-AUG-2000;
12-SEP-2000;
20-SEP-2000;
                                                                                                                        13-OCT-1999;
04-JAN-2000;
03-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bone morphogenetic protein-1; BMP-1; vascular endothelial growth factor; VBGF-8; platelet derived growth factor; VBGF, CCTRX; hyperplasia; cancer; neoplasia; anaemia; leukopenia; baldness; cardiovascular disorder; fibrotic disorder; diabetic ulcer; obesity; hyperproliferation; human; dysproliferation, neurodegenerative disorder; osteoarthritis; epilepsy; inflammatory disorder; Graft versus host disease; coagulation; haemophilia; neural disorder; Parkinson's disease; Alzheimer's disease; multiple sclerosis; Huntington's disease; amyotrophic lateral sclerosis;
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Best Local Sim:
Matches 370;
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N-PSDB; AAS04498.
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The sequence represents a protein related to bone morphogenetic protein-1 (BMP-1), vascular endothelial growth factor (VBGF-E) and platelet derived growth factor (PDGF). Polypeptides and polynucleotides related to BMP-1, VBGF-E and PDGF are referred to as FCTRX peptides and nucleic acids. FCTRX proteins are useful for treating or preventing a disorder associated with aberrant expression, aberrant processing, or aberrant physiological interactions of the proteins in a mammal, where the disorder is characterised by insufficient or ineffective growth of a cell or a tissue, e.g. hyperplasia or neoplasia. The peptides and their associated nucleic acids are useful for both promoting and inhibiting

Novel growth factor polypeptides termed as FCTRX polypeptides, useful for treating cancer, cardiovascular and fibrotic diseases, diabetic ulcers, wound healing and neuronal disorders.

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13-OCT-1999; 99US-0159231P.
04-JAN-2000; 2000US-0174485P.
03-MAR-2000; 2000US-01867707P.
10-MAR-2000; 2000US-0188250P.
08-AUG-2000; 2000US-023879P.
12-SEP-2000; 2000US-02662783.
20-SEP-2000; 2000US-0234082P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bone morphogenetic protein-1; BMP-1; vascular endothelial growth factor; VBGF-E; platelet derived growth factor; PDGF; FCTRX; hyperplasia; cancer; neoplasia; anaemia; leukopenia; baldness; cardiovascular disorder; fibrotic disorder; diabetic ulcer; obesity; hyperproliferation; human; dysproliferation, neurodegenerative disorder; osteoarthritis; epilepsy; inflammatory disorder; Graft versus host disease; coagulation; haemophilia; neural disorder; Parkinson's disease; Alzheimer's disease; multiple sclerosis; Huntington's disease; amyotrophic lateral sclerosis;
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13-OCT-1999;
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ncer; osteonecrosis; bone defect; osteogenesis; osteoporosis;
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The patent discloses materials and methods for reducing cell
CC proliferation or extracellular matrix production, treating fibrosis and
CC reducing stellate cell activation in a mammal. The method comprises
CC administering a composition containing a Zvegf3 antagonist in combination
CC with a delivery vehicle. The Zvegf3 is a protein that is structurally
CC related to platelet-derived growth factor (PDGF) and the vascular
CC endothelial growth factors (VEGF). The Zvegf3 protein is also designated
CC as "VEGF-R" and "PDGF-C". The Zvegf3 antagonist is useful to block the
CC mitogenic effects of zvegf3 and thereby to inhibit or prevent and treat
CC teloids, scleroderma, fibrotic disorders of liver such as chronic active
CC hepatitis, fulminant viral hepatitis, post necrotic cirrhosis and alpha-1
CC diabetic glomerulosclerosis, focal glomerulosclerosis, diabetic
CC diabetic glomerulosclerosis, focal glomerulosclerosis, diabetic
CC of the lung such as silicosis, and reriosclerosis, fibrotic disorders
CC fibrotic disorders of pancress, fibropoliferative
CC bronchiolitis obliterans-organising pneumonia and pulmonary hypertension,
CC fibrotic disorders of pancress, fibropoliferative disorders of the bone such as osteopetrosis and hyperoscosis. The present
CC disorders is human Zvegf4 protein which forms a heteromultimer with Zvegf3
CC received.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of zvegf3 antagonist for reducing fibroproliferative disorder kidney, liver and bone, reducing extracellular matrix production, treating fibrosis or reducing stellate cell activation in mammal.
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12-NOV-1999; 99US-0165255P
01-AUG-2000; 2000US-0222223P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 62-63; 70pp; English.
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04-FEB-2000; 2000US-0180628P
12-SEP-2000; 2000US-0231968P
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Best Local
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LP85; platelet-derived growth factor; PDGF; antiinflammatory; vulnerary; osteopathic; neuroprotective; tranquilliser; musculoskeletal disorder;
                                                                      Human LP85 protein #1
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11-JAN-2001;
11-JAN-2001;
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                                                                                                                                                                                                                                                                                 Sequence
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Fernandes
          The present sequence is the protein sequence of human growth factor FCTR1, or platelet derived growth factor D (PDGPD), a secreted protein that shows homology to human vascular endothelial growth factor E and to human PDGFs A, B and C. FCTR1 RNA is present in pituitary gland tissues, uterine microvascular endothelial cells, crybroleukaemia cells, thyroid, small intestine, lymphocytes, adrenal gland and salivary gland. The invention provides FGFCX and FCTRX growth factors, polypeptides and
                                                                                                                           Treating, delaying the onset of, or ameliorating an inflammatory pathology (e.g. inflammatory bowel disease or Crohn's disease) by administering to the subject fibroblast growth factors or a combination of growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FCTR1; platelet derived growth factor D; PDGFD; human; Crohn's disease; inflammatory bowel disease; gene therapy; antiinflammatory; vulnerary; cytostatic; cardiovascular.
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DB; ABN84524.
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RESULT 12
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XX ABG92892
XX ABG92
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XX UPGF;
KW UPGF;
KW Chrom
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metabolism;

stroke;

disease;

US6432673-B1

neurite

outgrowth.

13-AUG-2002

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                                                                                                                                                                                                                                                                                      CC vascular endotholial growth factor-like protein) of 111-136 amino acid cresidues in length and comprises the sequence appearing as ABG9289 from CC comprising a first polypeptide disulphide bonded to a second polypeptide, where each of the first and second polypeptides is from zvegf 3 and CC where each of the first and second polypeptides is from zvegf 3, and CC where the protein modulates cell proliferation, differentiation, cmetabolism or migration, the zvegf 3 encoding polynucleotides and zvegf 3 cxpression vectors and host cells. Zvegf 3 is useful as additives in CC for designing molecules that antagonise semaphorin-stimulated activities, including neurite growth, cardiovascular development, cartilage and limb CC sites of abnormal cell proliferation and in gene therapy applications. CC repair, or cellular differentiation or proliferation, for stimulating the growth of fibroblast or smooth muscle cells, as molecular weight correpair, or cellular differentiation or proliferation, for stimulating the growth of solid tumours, for treating diabetic retinopathy, for clibrosis, including scar formation, keloids, liver fibrosis, lung fibrosis, esticuses, as passes of cell proliferation, keloids, liver fibrosis, lung fibrosis, esticuses (hepatitis), cirrhosis, streat disease (hepatitis), cirrhosis, streat disease, and reducing consulting scar formation, keloids, liver fibrosis, lung fibrosis, cardiac sclerosis, neurodegenerative diseases, and for the consulting scar formation, keloids, liver fibrosis, lung fibrosis, cardiac sclerosis, send female reproductive tract disease, and reducing consulting scar formation, keloids, liver fibrosis, lung fibrosis, cardiac sclerosis, send female reproductive tract disease, and for regenerating neurite outgrowths following strokes. The gene for human consulting scar formosome 4928.3. The present sequence represents
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06-JUL-1999;
21-OCT-1999;
                                                                                                                                                                                                                                                                                    Sequence
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99US-0161653P.
99US-0165255P.
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RESULT 13
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        This sequences represents human zvegf4. zvegf4 can be used in a composition with either human or mouse zvegf3, for promoting growth of bone, ligament or cartilage and stimulating proliferation of osteoblasts or chondrocytes in a mammal. zvegf3 is a platelet derived growth factor (PDGF) homolog. The zvegf3 protein used was preferably a dimeric protein of residues 235-345 of human zvegf3 or all of the mouse zvegf3 protein, with a delivery vehicle. The method of thinvention is useful for promoting growth of bone, ligament or cartilage in a mammal, where the composition is administered at a site of a bony defect, purferably a fracture, bone graff site, implant site, or periodontal pocket, and for stimulating proliferation of osteoblasts or chondrocytes in a mammal. It
                                                                                                                                                                                                                                                                                                                                                                                                                           21-OCT-1999;
12-NOV-1999;
07-DEC-1999;
                                                                                                                                                                                                                                Promoting growth of bone, ligament or cartilage in a mammal, involves administering to the mammal a protein which comprises growth factor domain of zvegf3 protein, a homolog of platelet-derived growth factor.
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06-JUL-1999;
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Best Local Sim:
Matches 370;
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                                                                                                                                                                                                                                       Zvegf4; human; gene therapy.
                                                                                                                                                                                                                                                                        Human zvegf4 protein.
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                                                                                                                                                                                                                                                                                                                                      ABB79588 standard; protein;
26-OCT-2001; 2001WO-US050155
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                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                  kidney; acute tubular necrosis; nephrotropic;
                                                                                                                           /label= CUB_domain+interdomain+growth_factor_domainter= "alternatively comprises residues 24-370, 35-370 or 52-370"
                                                                      /label= Growth_factor_domain
/note= "alternatively comprises residues 250-370 or 258-
                                                                                                                                                            /label= Signal_peptide
                                                                                                                                                                                              Location/Qualifiers
                                                                                                       'label = Growth_factor_domain+Interdomain
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1 MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDESNHLTDLYRRDETIQVKG

MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDESNHLTDLYRRDETIQVKG

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CC growth factor domain having a cystine knot structure, and a CUB domain. A CC propeptide-like sequence extends from residue 180 to either residue 245. CC 249 or 257. Zvegf4 (2an thus be prepared in a variety of multimeric forms CC including zvegf4 (1258-370). zvegf4 (252-370). zvegf4 (256-370). zvegf4 (250-370) and zvegf4 (258-370). Expression of zvegf4 polynucleotide in cultured CC mammalian cells results in production of a disulfide-bonded, dimeric CC processing to remove the CUB and interdomain regions. An active growth CC factor domain dimer can be produced directly by expressing a truncated CC polynucleotide. A claimed method of improving kidney function, or CC enhancing proliferation or survival of kidney tubule epithelial cells or CC enhancing proliferation or survival of kidney tubule epithelial cells or CC epithelial cell precursors in a mammal, comprises administering a composition containing a zvegf4 protein or zvegf4 protein-encoding composition containing a zvegf4 protein or zvegf4 protein is preferably a disulfide bonded dimer of 2 polypeptide chains comprising residues 258-370, 250-250, 253, 254, 255, 256, 257, 258, 259, 259, 260, 261, 262 or 263, and y CC 244, 25, 35, 52, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, CC 246, 250, 253, 254, 255, 256, 257, 258, 259, 260, 261, 260 or 263, and y CC 253, 264, 267, 269 or 370 or 263, and y CC 254, 253, 264, 255, 256, 257, 258, 259, 259, 260, 261, 262 or 263, and y CC 253, 264, 267, 268, 267, 268, 257, 258, 259, 260, 261, 262 or 263, and y CC 253, 264, 253, 264, 255, 256, 257, 258, 259, 259, 260, 261, 262 or 263, and y CC 253, 264, 267, 268, 267, 268, 267, 268, 269, 260, 261, 262 or 263, and y CC 253, 264, 267, 268, 267, 268, 269, 260, 261, 262 or 263, and y CC 253, 264, 267, 268, 267, 268, 267, 268, 267, 268, 267, 268, 267, 268, 267, 268, 267, 268, 267, 268, 267, 268, 267, 268, 267, 268, 267, 268, 267, 268, 267, 268, 267, 268, 267, 268, 267, 268, 267, 268, 267, 268, 267, 268, 267, 268, 267, 268, 267, 268, 267, 268, 267, 268, 267, 268, 267, 
                      Query Match
Best Local
  Matches 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 predictions suggest the polypeptide can form homomultimers or heteromultimers that act on tissues by modulating cell proliferation, migration, differentiation or metabolism. The polypeptide compirses a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is the protein sequence of human vegf4, a protein which activates the alpha-alpha, alpha-beta and beta-beta forms of the platelet-derived growth factor (PDGF) receptor. Zvegf4 is structurally related to PDGF and vascular endothelial growth factor. Structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Improving kidney function, or enhancing proliferation or survival or kidney tubule epithelial cells or epithelial cell precursors in a maccomprises administering a zvegf4 protein or zvegf4 protein-encoding
                                                                                                            Sequence 370
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100.0%; Score 370; I
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 370 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 11-13; 177pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting presence or amount of 30664188 antigen in a sample, by contacting the biological sample with agent that binds the antigen, detecting the presence or amount of agent bound to the antigen.
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                                              ETST1 IRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLEDFQPAAASE
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(MOOR/)
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New secreted polypeptides and preventing, treating and diagr
                              WPI; 2002-608160/65.
N-PSDB; ABS58475.
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12-SEP-2000;
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BIRSE C E.
SOPPET D R.
OLSEN H S.
MOORE P A.
WEI P.
EBNER R.
DUAN D R.
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                                                         Komatsoulis GA,
Moore PA, Wei
M, Ni J, Ruben
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 s and encoding polynucleotides, undiagnosing diseases e.g. anemia,
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p, Ebner R,
M, Barash S
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diabetes,

asthma, psoriasis, Parkinson's and

Alzheimer'

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RESULT 17
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ID ABG64
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AC ABG64
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CC or expression of the protein The sequences are useful for identifying a
CC binding partner to the protein comprising contacting the protein with a
CC binding partner and determining whether the binding partner effects an
CC or ameliorating a medical condition such as an autoimmune disease (e.g.
CC multiple sclerosis, myasthenia gravis), blood coagulation disorders (e.g.
CC fibrinogenaemia, haemophilia), blood platelet disorders (e.g.
CC thrombocytopenia), hyperproliferative disorders (e.g. sarcoidosis, Sezary
CC syndrome), neurodegenerative disorders (e.g. Alzheimer's disease,
CC parkinson's disease), renal disorders (e.g. Alzheimer's disease,
CC parkinson's consilitis, laryngitis), endocrine disorders (e.g.
CC disorders (e.g. tonsilitis, laryngitis), endocrine disorders (e.g.
CC acromegaly, thyrotoxicosis), reproductive disorders (gonorrhea,
CC stenosis), infectious diseases (e.g. polio, rubella) and cancer.
CC sequences ABG76569-ABG76616 represent human secreted proteins of the
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                                                       Human albumin
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Albumin fusion protein; therapeutic
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                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to albumin fusion proteins comprising a therapeutic protein x and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and disgnosing disorders such as cancer, reproductive disorders dispetive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetcs), haematopoietic disorders, neural disorders (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention
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25-APR-2000; 2000US-0199384P
21-DEC-2000; 2000US-0256931P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human serum albumin; HSA; cancer; reproductive disorder; disestive disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disocytostatic; antiinfertility; antiinflammatory; antiuncer; immunomodulator; anti-HIV; antidiabetic; haemostatic; noo neuroprotective; antiparkinsonian; antimicrobial; neurole
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                       1 MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDESNHLTDLYRRDETIQVKG
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LDTPRYKGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQ
                                                  TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMY
                                                                     TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMY
                                                                                                                  ETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLEDFQPAAASE
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Pred. No. 0;
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301

RCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC

LDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQ

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The present invention describes a method for reducing proliferation of or cettracellular matrix production by a cell in a mammal. The method CC comprises administering to the mammal a composition comprising a CC therapeutically effective amount of a zvegf4 antagonist chosen from anti-cvegf4 antibodies, inhibitory polynucleotides, inhibitors of zvegf4 cotivation, and mitogenically inactive, receptor-binding variants of cvegf4. Zvegf4 (also called PDGF-D) is a multi-domain protein that is cructurally related to platelet derived growth factor (PDGF) and CC vascular endothelial growth factors (VEGF). Zvegf4 has cytostatic, CC emphrotropic, hepatotropic, antiinflammatory, osteopathic and CC antiarthritic activities. The method is useful for reducing proliferation of mesangial, epithelial, endothelial, smooth muscle, fibroblast, CC in a mammal, in particular proliferation of prostate tumour cells, and CC in a mammal, in particular proliferation of prostate tumour cells, and cfor reducing extracellular matrix production by a cell in a mammal cc suffering from a fibroproliferative disorder of kidney, bone or liver. In particular it is useful for reducing stellate cell activation. The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 19-20; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reducing
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03-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prostate tumour; prostate cancer; glomerulonephritis; lupus nephritis; diabetic glomerulosclerosis; renal arteriosclerosis; nephrotic syndrom chronic active hepatitis; cirrhosis; osteopetrosis; osteosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; zvegf4; cell proliferation; extracellular matrix production; fibroproliferative disorder; PDGF-D; platelet derived growth factor; PDGF; vascular endothelial growth factor; VEGF; cytostatic; nephrotropic; hepatotropic; antiinflammatory; osteopathic; antiarthritic; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          g proliferation or extracellular matrix production by a cell in useful for treating fibroproliferative disorders of bone, liver ney, comprises administering a zvegf4 antagonist.
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TOPOUZIS
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Query Match
Best Local
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                                                                                                                                                                                                                                                            Human; growth factor homologue; ZVBGP4; proliferation; differentiation; migration; mesenchymal cell; call; esemphorin; neuropilin; neurite growth; cardiovascular development; limb development; carcilege development; T-cell; B-cell; rheumatoid arthritis; cancer;
                                                                                                                                                                                                                                         autoimmune disease; inflammation; retinopathy; haemangioma;
                                                                                                                                                                                                                                                                                                                                                                           Human growth
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                                                                                                                                                                                                                                                                                                                                                     protein stimulates proliferation, differentiation, or migration of the mesenthymal cells and may modulate activities mediated by cell surface semaphorins. ZVEGF4 may be used to design ant/agonists of neuropilingemaphorin interactions which may be of use in neurite growth, cardiovascular development, cartilage and limb development, T- and B-cell functions as well as treating rheumatoid arthritis, various forms of cancer, autoimmune diseases, inflammation, retinopathies, haemangiomas, ischaemic events, neuropathies, acute nerve damage, central nervous system diseases and peripheral nervous system diseases including stroke. The isolated protein is also used for a pharmaceutical composition as therapeutic agents, diagnostic agents, and research tools and reagents. It can be used in the study and regulation of cell and tissue development, as components of cell culture media. The proteins can form homomultimers or heteromultimers that act on tissues to control organ development by modulating cell proliferation, migration, differentiation, or metabolism. The gene for human ZVEGF4 is located on chromosome 11q22.3
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10-NOV-1999;
04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated growth factor analogue ZVEF4 proteins for pharmaceutical composition as, e.g. therapeutic agents, diagnostic agents, and research tools and reagents, includes polypeptides from amino acid residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated protein comprising a first polypeptide disulphide-bonded to a second polypeptide. The first and second polypeptides are from 113-138 amino acid residues and comprises 258-370 amino acid residues of human growth factor homologue ZVEGF4. The second polypeptides are from 113-138 amino acid residues of human growth factor homologue ZVEGF4. The second polypeptides are from 113-138 amino acid residues of human growth factor homologue ZVEGF4. The second polypeptides are from 113-138 amino acid residues of human growth factor homologue zvectors.
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                                                                                     New isolated zvegf3 polypeptide, useful for treating cancer, Alzheimer's disease, Parkinson's disease, chronic active hepatitis, hepatic vein thrombosis, comprises growth factor domain and CUB domain.
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Nervous system; platelet-derived growth factor; PDGF; psychosis; vascular endothelial growth factor; VEGF; neural; stem cell; me:nory; progenitor cell; neurodegeneration; ischaemia; neurological trauma; progenitor cell; neurodegeneration; ischaemia; neurological trauma; neuropsychiatry; learning; parkinson's disease; Huntington's disease; Amyotrophic Lateral Sclerosis; spinal ischaemia; ischaemic stroke; spinal cord injury; cancer-related; schizophrenia; Alzheimer's disease; depression; anxietty, phobia; stress; cognitive function; aggression; drug; alcohol; abuse; obsessive compulsive behaviour; proliferation; seasonal mood disorder; personality disorder; cerebral palsy; multi-infarct; dementia; Lewy body; age related; geriatric; growth; epilepsy; brain injury; multiple sclerosis; autism; differentiation; attention deficit disorder; narcolepsy.
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WO2003024478-A1

19-SEP-2002; 2002WO-IB003998

28-SEP-2001; 19-SEP-2001; 2001US-0323381P 2001US-0326044P

Zhao Z 7 Janson AM, Kuhn GH, Plate <u>,</u>~ Schanzer A, Wachs

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N-PSDB; ABQ80246

Use of platelet-derived growth factor, vascular endothelial growth factor, or their modulators for modulating neural stem cell or neural progenitor cell activity, particularly for treating e.g. Alzheimer's, ischemia or stroke.

Disclosure; Page 23; 119pp; English.

The sequences given in ABB80131-35 show proteins which may be used in the method of the invention for alleviating or reducing a symptom of a CC disease or disorder of the nervous system. The method comprises administering platelet-derived growth factor (PDGF), vascular endothelial growth factor (VEGF), a combination of PDGF and VEGF, or a PDGF or VEGF agonist, to a patient in order to endothate neural stem cell or neural corresponding the symptoms of a disease or disorder of the nervous system, and the symptoms of a disease or disorder of the nervous system, are reducing the symptoms of a disease or disorder of the nervous system, and the symptoms of a disease or disorder of the nervous system, are reducing the symptoms of a disease or disorder of the nervous system, are reducing the symptoms of a disease or disorder of the nervous system, are reducing the symptoms of a disease or disorder of the nervous system, are reducing the symptoms of a disease or disorders, neural stem cell disorders, neural properties of the nervous system, and the properties of the nervous system, and the memory of disorders. In particular, the method is useful for alleviating or treating parkinson's disease and disorders, Huntington's disease, and the stocker, spinal ischaemia, and other psychoses, depression, bipolar cold injury, schizonder, anxiety syndromes/disorders, phobias, stress and related syndromes, compulsive behaviour syndromes, seasonal mood disorder, borderline personality disorder, cerebral palsy, life style drug, multi-infarct dementia, Lewy body dementia, age related/geriatric conformation related brain/spinal cord injury, anti-cancer treatment related brain/spinal cord injury, infection and cord injury, anti-cancer treatment related brain/spinal cord injury, environmental toxin the manufacture of a medicament for alleviating or treating or treating or sleep disorders. The pDGF and/or vEGF, is useful in the manufacture of a medicament for alleviating or treating.

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                 WPI; 2003-421322/39
N-PSDB; ACC47941.
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New protein consisting of two platelet-derived growth factor-D polypeptide chains, useful for stimulating the production of bone and/or connective tissue in both humans and animals, e.g. in treating fractures
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English.

The invention relates to a protein consisting of two platelet-derived growth factor-D (PDGF-D) polypeptide chains. The protein is useful in enhanced production of PDGF-D growth factor domain dimers. It may be used to stimulate production of bone and/or connective tissue in both humans and animals, such as in cases of fractures, bone grafts, implants, repair of bony defects arising from surgery, surgical reconstruction following traumatic injury, repair of hereditary or other physical abnormalities, or in treatment of osteoporosis. The present sequence represents a human

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NGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRYDFVEVEDIS
RCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC
                   RCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC
                                                               LDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVEFPRCLLVQ
                                                                                           LDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQ
                                                                                                                                  TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMY
                                                                                                                                                     TNWESYTSSISGVSYNSPSYTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMY
                                                                                                                                                                                                   ETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLEDFQPAAASE
                                                                                                                                                                                                                      ETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLEDFQPAAASE
                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 370; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
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protein; 370

entry)

derived growth factor (PDGF-D)

Human; platelet-derived growth factor-D; PDGF-D; bone graft; osteopathic; radiation-induced osteonecrosis; periodontal disease; protein therapy; joint injury; osteoporosis; bone loss; fracture; bone healing. /note= "Secretory peptide" 52. .179 /note= "CUB domain" Location/Qualifiers

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Best Local S
Matches 370
                                                                                                                                                                                                                                                                                                                                                   The invention relates to a fusion protein comprising, from amino to carboxyl terminus, a first platelet-derived growth factor-D (PDGF-D) domain polypeptide, a linker polypeptide, and a second PDGF-D domain polypeptide. The fusion proteins are useful for stimulating the production of bone and/or connective tissue in both human and non-human animals. The fusion proteins are specifically useful in non-union fractures and fractures in patients with compromised healing, bone grafts, bone healing following radiation-induced osteonecrosis, implants, or treatment of periodontal disease, joint injuries, osteoporosis or other conditions characterised by increased bone loss or decreased bone formation. The invention is useful in protein therapy. The present requence is human platelet derived growth factor (PDGF-D). PDGF-D is
                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New fusion protein comprising a first platelet-derived growth factor-D (PDGF-D) domain, a linker, and a second PDGF-D domain polypeptides, useful for stimulating the production of bone and/or connective tissue.
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             LDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQ
                                                  TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMY
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Query Match
Best Local Similarity
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10-NOV-1999;
04-FEB-2000;
                                           The present invention relates to a method for promoting growth of bones ligaments and cartilages in a mammal. The invention is useful for treating osteoporosis such as age related osteoporosis, host-menopausal osteoporosis, glucocorticoid induced osteoporosis and disuse osteoporosis. The invention is also useful in treating bony defects due to injury, surgery, tumour removal, ulceration, infection or other congenital defects. The present sequence is human zvegf4 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
                             Sequence
                                                                                                                        Claim
                                                                                                                                         Method for promoting growth of bones, ligaments and cartilages in mammal, involves administering composition containing zvegf4 in vehicle.
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99US-0164463P.
2000US-0180169P.
2000US-00540224.
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06-JUL-1999;
21-OCT-1999;
12-NOV-1999;
07-DEC-1999;
31-MAR-2000;
                                                                                             Gao Z, Hai
Gilbertson
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                                                                                                                                                                                                                                                                                       Human zvegf3
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                                 Promoting wound healing or proliferation of fibroblasts or smooth muscle cells in a mammal, by administering a polypeptide comprising growth factor domain of human growth factor homolog polypeptide, zvegf3.
                                                                                                                                                                                                     06-NOV-2000; 2000US-00706968
                                                                                                                                                                                                                     04-MAR-2003
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                   Disclosure;
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 present invention relates to a method of
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DB; ADG47745.
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Matches 370;
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 370
361
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                 DCICSSRPPR
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                                                           RCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC
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ALIGNMENTS

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        Sequence 2, Application US/09540224

Patent No. 6468543

GENERAL INFORMATION:
APPLICANT: Gilbertson, Debra G.
APPLICANT: Hart, Charles E.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONI
TITLE OF INVENTION: LICAMENT AND CARTILAGE USING ZVEGF4

FILE REFERENCE: 00-28

FILE REFERENCE: 00-28
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Best Local S
Matches 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-60
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CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOPTWARE: FastSEQ for Windows Version 3.0
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ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 370
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; TYPE: PRT
; ORGANISM: Homo s
US-09-540-224-2
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EARLIER APPLICATION WUMBER: US 60/180,
EARLIER FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 2
LENGTH: 370
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GENERAL INFORMATION:
 Best Local Similarity Matches 370; Conserv
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                            Query Match
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APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
                                                                       LENGTH: 370
TYPE: PRT
ORGANISM: Homo
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Local Similarity 100.0%;
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RESULT 4
US-09-706-968-37
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Best Local Similarity
Matches 370; Conserv
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                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Homo sapiens -09-706-968-37
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APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-60C1
CURRENT APPLICATION NUMBER: US/09/706,968
CURRENT FILING DATE: 2000-11-06
PRIOR APPLICATION NUMBER: US/09/541,752
PRIOR FILING DATE: 2000-03-31
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APPLICANT: Hart, Char
APPLICANT: Piddington
APPLICANT: Sheppard,
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Sheppard, Paul O.
Shemaker, Kimberly E.
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CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US 60/235,295
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/164,250
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/132,250
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
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LENGTH: 370
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Patent No. 6630142
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 370; Best Local Similarity 100.0%; Pred. No. 0; Matches 370; Conservative 0; Mismatches
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APPLICANT: Topouzis, Stavros
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: 00-79
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Sequence 5, Application US/09823033

; Sequence 5, Application US/09823033

; Patent No. 6663870

; GENERAL INFORMATION:

; APPLICANT: Hart, Charles E.

APPLICANT: Gilbertson, Debra G.

TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF

TITLE OF INVENTION: LIGAMENT AND CARTILAGE

; FILE REFERENCE: 00-12

; CURRENT APPLICATION NUMBER: US/09/823,033

; CURRENT FILING DATE: 2001-03-29

; NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 5

; SEQ ID NO 5

; LENGTH: 370

TYPE: PRT

; ORGANISM: Homo sapiens
Sequence 8, Application US/09438046
PATENT NO. 6706687
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: LEE, Xuri
APPLICANT: LEE, Xuri
APPLICANT: UTFELA, Marko
APPLICANT: UTFELA, Marko
APPLICANT: OESTMAN, Arne
APPLICANT: OESTMAN, Arne
APPLICANT: HELDIN, Carl-Henrik
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Pred. No. 0;
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TITLE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REFERENCE: Ulf Eriksson et al 1064-44833
CURRENT APPLICATION NUMBER: US/09/438,046
CURRENT FILING DATE: 1999-11-10
EARLIER APPLICATION NUMBER: 60/107,852
EARLIER FILING DATE: 1999-11-10
EARLIER FILING DATE: 1999-12-28
EARLIER APPLICATION NUMBER: 60/113,997
EARLIER APPLICATION NUMBER: 60/150,604
EARLIER FILING DATE: 1999-08-26
EARLIER FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: 60/157,108
EARLIER APPLICATION NUMBER: 60/157,756
EARLIER APPLICATION NUMBER: 60/157,756
EARLIER APPLICATION NUMBER: 60/157,756
EARLIER FILING DATE: 1999-10-05
NUMBER: DATE: 1999-10-05
NUMBER: DATE: 1999-10-05
NUMBER: DATE: 1999-10-05
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                                                                      GENERAL INFORMATION:

APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: West, Kimberly E.
APPLICANT: West, James W.

TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
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Best Local Similarity
Matches 370; Conserv
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SEQ ID NO 8
LENGTH: 370
                  FILE REFERENCE: 98-60
CURRENT APPLICATION NUMBER: US/10/139,583
CURRENT FILING DATE: 2002-05-02
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ORGANISM: Homo
    APPLICATION NUMBER:
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Topouzis, Stavros
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING
TITLE OF INVENTION: KIDNEY FUNCTION
FILE REFERENCE: 00-100
CURRENT APPLICATION NUMBER: US/10/039,847A
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: US 60/244,479
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; PRIOR FILING DATE: 1999-12-07; NUMBER OF SEQ ID NOS: 50; SOFTWARE: FastSEQ for Windows Volume 1997 (SEQ ID NO 37; ENGTH: 370; TYPE: PRI ORGANISM: HOMO Bapiens US-10-139-583-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
US-10-039-847A-2
                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches
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APPLICANT: AASE, Karin
APPLICANT: LEE, Xuri
APPLICANT: UTELA, Warko
APPLICANT: UTELA, Marko
APPLICANT: HELDIN, Carl-Henrik
ITILE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, I
ITILE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, I
ITILE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REFERENCE: Ulf Eriksson et al 1644-44833
CURRENT FILING DATE: 1999-11-10
EARLIER APPLICATION NUMBER: 60/107,852
EARLIER APPLICATION NUMBER: 60/107,852
EARLIER FILING DATE: 1999-11-10
EARLIER FILING DATE: 1999-11-10
EARLIER APPLICATION NUMBER: 60/150,604
EARLIER APPLICATION NUMBER: 60/157,108
EARLIER APPLICATION NUMBER: 60/157,108
EARLIER APPLICATION NUMBER: 60/157,108
EARLIER FILING DATE: 1999-10-04
EARLIER FILING DATE: 1999-10-04
EARLIER FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 6
LENGTH: 322
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 322; Conserv
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169 LLEDFQPAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFN
                                                                                                                                        49 LYRRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEBAENDI
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                                                                                                                 1 LYRRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDI
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y 100.0%; Pr
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Pred. No. 2.5e-305;
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RESULT 12
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APPLICANT: Gilbert, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 60/164,463
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US-09-564-595D-56
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                                                    Sequence 55, Application Patent No. 6495668 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 56
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Best Local
APPLICANT: Gilbert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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100.0%; Pred. No. 2.5e-193;
                                                                                           US/09564595D
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APPLICANT: Hart, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FAStSEQ for Windows Version 4.0
SEQ ID NO 57
LENGTH: 303
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FILE REPERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-0
PRIOR FILING DATE: 1999-11-0
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 55
LENGTH: 316
TYPE: PRT
ROANIEM: Artificial Sequence
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                                                                                     ; FEATURE:
; OTHER INFORMATION:
US-09-564-595D-57
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US-09-564-595D-57
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Query Match
Best Local Similarity
Matches 128; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 51.6%;
Best Local Similarity 100.0%;
Matches 191; Conservative
                                                                                                                                               ORGANISM: Artificial Sequence
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHER
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                                                                                                         fusion polypeptide
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34.6%; Score 128; DB 4; L
100.0%; Pred. No. 2.1e-116;
tive 0; Mismatches 0;
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                                          DB 4; Length 303;
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Conservative

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Gaps

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GENERAL INFORMATION:

APPLICANT: EARIS, KARIN

APPLICANT: LEE, XURI

APPLICANT: LEE, XURI

APPLICANT: LEE, XURI

APPLICANT: LEE, XURI

APPLICANT: PONTN, Annica
APPLICANT: PONTN, Annica
APPLICANT: PONTN, Annica
APPLICANT: HELDIN, CARI-Henrik

TITLE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REFERENCE: U1f ERIKSSON et al 1064-44833

CURRENT APPLICATION NUMBER: 60/107,852

EARLIER FILING DATE: 1999-11-10

EARLIER APPLICATION NUMBER: 60/113,997

EARLIER APPLICATION NUMBER: 60/13,997

EARLIER APPLICATION NUMBER: 60/150,604

EARLIER FILING DATE: 1999-10-64

EARLIER FILING DATE: 1999-10-70

EARLIER FILING DATE: 1999-10-64

EARLIER FILING DATE: 1999-10-64

EARLIER FILING DATE: 1999-10-64

EARLIER FILING DATE: 1999-10-04

EARLIER APPLICATION NUMBER: 60/157,708

EARLIER FILING DATE: 1999-10-04

EARLIER APPLICATION NUMBER: 60/157,708

EARLIER FILING DATE: 1999-10-05

NUMBER OF SEQ ID NOS: 31

SOFTMARE: PATENTIN PATENT PATENTIN PATENT
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US-09-438-046-4
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US-09-438-046-19
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US-09-438-046-19
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                                                                                                          Sequence 4, Application US/09438046
Patent No. 6706687
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: AASE, Karin
APPLICANT: LEE, Xuri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 32.2%; Score 119; DB 4; Length 119; Best Local Similarity 100.0%; Pred. No. 5.5e-108; Matches 119; Conservative 0; Mismatches 0; Indels
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Patent No. 6706687
APPLICANT: PONTN, Annica
APPLICANT: UUTELA, Marko
APPLICANT: ALITALO, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 DFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 DEOPAAAS 179
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APPLICANT: OESTWAN, Arne
APPLICANT: HELDIN, Carl-Henrik
TITLE OF INVENTION: CARL-HEREVED GROWTH FACTOR D,
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REFERRINCE: Ulf Eriksson et al 1064-44833
CURRENT APPLICATION NUMBER: US/09/438,046
CURRENT FILING DATE: 1999-11-10
EARLIER FILING DATE: 1999-11-0
EARLIER APPLICATION NUMBER: 60/107,852
EARLIER APPLICATION NUMBER: 60/113,997
EARLIER FILING DATE: 1999-12-28
EARLIER FILING DATE: 1999-12-28
EARLIER FILING DATE: 1999-10-06
EARLIER FILING DATE: 1999-10-06
EARLIER FILING DATE: 1999-10-05
EARLIER APPLICATION NUMBER: 60/157,108
EARLIER APPLICATION NUMBER: 60/157,756
EARLIER APPLICATION NUMBER: 60/157,756
EARLIER APPLICATION NUMBER: 60/157,756
EARLIER APPLICATION NUMBER: 60/157,756
EARLIER APPLICATION SUMBER: 60/157,756
EARLIER APPLICATION S
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APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-02-04
NUMBER OF 52G ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 54
LENGTH: 302
                                                                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: fusion polypeptide US-09-564-595D-54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 54, Applicat Patent No. 6495668 GENERAL INFORMATION:
                                                                                                                                                                         Query Match 30.5%; Score 113; DB 4; L
Best Local Similarity 100.0%; Pred. No. 8.5e-102;
Matches 113; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 31.6%; Score 117; DB 4; Louis Local Similarity 100.0%; Pred. No. 7.6e-106; Matches 117; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                            258 VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 YNSPSYTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMYLDTPRYRGRSYHDR
190 VDLDRLNÓDAKRYSCTÞRNYSVNÍREELKLANVVFFÞRCLLVQRCGGNCGCGTVNWRSCT
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                                                                                                                                                                                                                                                                  Length 302;
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TITLE OF INVENTION: CHARLET-DERIVED GROWTH FACTOR D, ITTLE OF INVENTION: THEREFOR, AND USES THEREOF FILE REFERENCE: UIf Eriksson et al 164-44833 CURRENT APPLICATION NUMBER: US/09/438,046 CURRENT FILING DATE: 1999-11-10

EARLIER APPLICATION NUMBER: 60/107,852

EARLIER FILING DATE: 1998-11-10

EARLIER FILING DATE: 1998-11-10

EARLIER APPLICATION NUMBER: 60/113,997

EARLIER FILING DATE: 1999-12-28

EARLIER FILING DATE: 1999-12-28

EARLIER FILING DATE: 1999-13-26

EARLIER FILING DATE: 1999-13-26

EARLIER FILING DATE: 1999-10-04

EARLIER APPLICATION NUMBER: 60/157,756

EARLIER APPLICATION NUMBER: 60/157,756

EARLIER FILING DATE: 1999-10-05

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PATENTIN Ver. 2.0
            APPLICANT: ERIKSSON, Ulf
APPLICANT: AASE, Karin
APPLICANT: LEE, Xuri
APPLICANT: DONTN, Annica
APPLICANT: UUTELA, Marko
APPLICANT: HELDIN, Cari-Henrik
APPLICANT: HELDIN, Cari-Henrik
APPLICANT: HELDIN, Cari-Henrik
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D,
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REFERENCE: Ulf Eriksson et al 1064-44833
CURRENT APPLICATION NUMBER: US/09/438,046
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; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-438-046-2
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US-09-438-046-2
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US-09-438-046-18
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APPLICANT: AASE, Karin
APPLICANT: LEE, Xuri
APPLICANT: PONTN, Annica
APPLICANT: UUTELA, Marko
APPLICANT: ALITALO, Kari
APPLICANT: OESTWAN, Arne
APPLICANT: HELDIN, Carl-Henrik
APPLICANT: HELDIN, Carl-Henrik
                                                                                                                                                                                                                                                       Sequence 18, Applica Patent No. 6706687 GENERAL INFORMATION:
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NO. 6706687
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; Pred. No. 1.4e-5
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-438-046-18
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US-09-564-595D-53
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                                                                                                              Sequence 53, Application US/09564595D Patent No. 6495668 GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 27; Conservative (
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LENGTH: 370
TYPE: PRT
ORGANISM: Mus musculus
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SEQ ID NO 18
LENGTH: 121
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              APPLICANT: Gilbert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
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APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Hart, Charles E.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
FILE REFERENCE: 00-28
CURRENT APPLICATION NUMBER: US/09/540,224
CURRENT FILING DATE: 2000-03-31
EARLIER APPLICATION NUMBER: US 60/180,169
EARLIER APPLICATION WIMBER: US 60/180,169
ANUMBER OF SEC ID NOS: 9
SOFTMARE: FastSEQ for Windows Version 3.0
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EARLIER FILING DATE: 1998-11-10
EARLIER APPLICATION NUMBER: 60/113,997
EARLIER FILING DATE: 1999-12-28
EARLIER FILING DATE: 1999-12-28
EARLIER FILING DATE: 1999-150,604
EARLIER FILING DATE: 1999-00-26
EARLIER APPLICATION NUMBER: 60/157,766
EARLIER APPLICATION NUMBER: 60/157,756
EARLIER FILING DATE: 1999-10-05
EARLIER FILING DATE: 1999-10-05
NUMBER: 05/157,756
EARLIER FILING DATE: 1999-10-05
NUMBER: 05/157,756
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142 SRTNQIKITFKSDDYFVAKPGFKIYYS 168
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                                                                                                        7.3%; Score 27; DB 4; Lo
100.0%; Pred. No. 5.8e-18;
lve 0; Mismatches 0;
                                                                                                                                                              Length 370;
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; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-808-972-4
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US-09-808-972-4
                                                                                                                                                                    RESULT 22
US-10-039-847A-4
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CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US 60/235,295
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/564,595
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR APPLICATION NUMBER: US 60/164,250
PRIOR APPLICATION NUMBER: US 60/132,250
PRIOR APPLICATION NUMBER: US 60/132,250
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 27
  Sequence 4, Application US/10039847A
PACENT NO. 6827938
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: TOPOUZIS, Stavros
TITLE OF INVENTION: KIDNEY FUNCTION
TITLE OF INVENTION: KIDNEY FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 53
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Best Local Similarity
Matches 27; Conserv
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SEQ ID NO 4
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APPLICANT: Topouzis, Stavros
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
FILE REFERENCE: 00-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
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PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1999-05-03
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TYPE: PRT
ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                          142 SRTNQIKITFKSDDYFVAKPGFKIYYS 168
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100.0%; Pred. No. 5.8e-18;
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100.0%; Pred. No. 5.8e-18;
1ve 0; Mismatches 0;
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                             METHODS
                             FOR IMPROVING
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CURRENT APPLICATION NUMBER: US/10/039,847A
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: US 60/244,479
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 370
TYPE: PRT
APPLICANT: Gilbert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR APPLICATION NUMBER: US 60/164,169
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 2000-02-04
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PATENT NO. 6468543
GENERAL INFORMATION:
APPLICANT: Glibertson, Debra G.
APPLICANT: Hart, Charles E.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
FILE REFERENCE: 00-28
                                                                                                                                                                                                                                                                                                        Sequence 40, Application US/09564595D Patent No. 6495668 GENERAL INFORMATION:
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LENGTH: 25
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Best Local Similarity 100.0%; P
Matches 27; Conservative 0;
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Best Local Similarity
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CURRENT FILING DATE: 2000-03-31
EARLIER APPLICATION NUMBER: US 60/180,169
EARLIER FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
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ORGANISM: Artificial Sequence
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100.0%; Pred. No. 4.9e-1
/ative 0; Mismatches
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100.0%; Pred. No. 5.8e-18;
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GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
TITLE OF INVENTION: MISORDERS
FILE REFERENCE: 00.79
CURRENT APPLICATION NUMBER: US/09/808,972
CURRENT APPLICATION NUMBER: US 60/235,295
PRIOR APPLICATION NUMBER: US 09/564,595
PRIOR APPLICATION NUMBER: US 09/564,595
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 25
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
FORMATION: peptide
US-09-808-972-10
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; SOFTWARE: FRASTSEQ for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-09-564-595D-40
Search completed: November 10, 2005, 09:48:22 Job time : 44 secs
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Perfect score:
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1: /cgn2=6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2=6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

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2 US-10-086-623-8

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Sequence 2, Appli
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Sequence 2, Appli
Sequence 1482, Appli
Sequence 8, Appli
Sequence 37, Appli
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   S-10-365-095-2

S-10-321-962-4

S-10-606-055-2

S-10-664-432-5

S-10-650-284-2
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S-10-274-638-2
S-10-011-364-4
S-10-277-802-56
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APPLICANT: HART, Charles E.
APPLICANT: HART, Charles E.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BON
TITLE OF INVENTION: LIGAMENT AND CARTILAGE
FILE REFERENCE: 00-12
CURRENT APPLICATION NUMBER: US/09/823,033
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
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Patent No. US20020004225A1
GENERAL INFORMATION:
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Best Local
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                                                     RCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC
                                                                                   LDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQ
                                                                                                           TWWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKXFNPESWQEDLENMY
                                                                                                                      TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMY
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                          DCICSSRPPR
                                          RCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC
                                                                          LDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQ
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US-10-123-215-186
US-10-123-902-186
US-10-123-909-186
US-10-123-910-186
US-10-124-813-186
US-10-124-813-186
US-10-124-813-186
US-10-125-922-186
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Pred. No. 0;
0; Mismatches
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US-09-915-582-56
US-09-915-582-56
; Sequence 56, Application US/
; Patent No. US20020120103A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Huma
; FILE REFERENCE: PS723P1
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CURRENT APPLICATION NUMBER: US/09/808,972
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US 60/235,295
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/564,595
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1909-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/132,250
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 370
TYPE: PAT
ORGANISM: Homo sapiens
US-09-808-972-2
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Patent No. US20020064832A1
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Topouzis, Stavros
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHOD OF TR
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: 00-79
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Similarity 100.0%;
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Pred. No. 0;
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US-09-876-813-2

US-09-876-813-2

Sequence 2, Application US/09876813

Publication No. US20040002140A1

GENERAL INFORMATION:
APPLICANT: Glabert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19

CURRENT APPLICATION NUMBER: US/09/876,813

CURRENT FILING DATE: 2000-05-03

PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1999-05-03

PRIOR FILING DATE: 1999-05-03

PRIOR FILING DATE: 1999-11-10

PRIOR FILING DATE: 1999-11-10

PRIOR FILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 57

SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/915,582
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: PCT/US01/01431
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-12
PRIOR APPLICATION NUMBER: 60/231,968
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 97
SOCTWARE: PATE, 1005
SEQ ID NO 56
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Simi
Matches 370;
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TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1482
LENGTH: 370
TYPE: PRT
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Publication No. US20040010134A1
GENERAL INFORMATION:
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LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
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        NGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRYDFVEVEDIS
                                                                                            MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDESNHLTDLYBRDETIQVKG
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                                                                        MHRLI FVYTLI CANFCSCRDTSATPQSASIKALRNANLRRDESNHLTDLYRRDETIQVKG
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; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo s
US-10-086-623-8
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APPLICANT: AASE, Karin
APPLICANT: AASE, Karin
APPLICANT: DON'EN, Annica
APPLICANT: PON'EN, Annica
APPLICANT: UTELA, Marko
APPLICANT: UTELA, Marko
APPLICANT: UTELA, Marko
APPLICANT: UTELA, Marko
APPLICANT: HELDIN, Carl-Henrik
TITLE OF INVENTION: PLATELET DERIVED GROWTH FAC
FILE REFERENCE: 1064/44833C2
CURRENT FILING DATE: 2000-03-04
PRIOR APPLICATION NUMBER: US 60/107,852
PRIOR APPLICATION NUMBER: US 60/107,852
PRIOR APPLICATION NUMBER: US 60/113,997
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-10-04
PRIOR APPLICATION NUMBER: US 60/150,604
PRIOR APPLICATION NUMBER: US 60/157,108
PRIOR APPLICATION NUMBER: US 60/157,756
PRIOR APPLICATION NUMBER: US 60/157,756
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 09/438,046
PRIOR APPLICATION NUMBER: US 09/438,046
PRIOR APPLICATION NUMBER: US 09/438,046
PRIOR APPLICATION NUMBER: US 09/691,200
PRIOR APPLICATION NUMBER: US 09/691,200
PRIOR FILING DATE: 2000-10-19
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                                                                                                                                                                                                              Query Match 100.0%; Score 370; I Best Local Similarity 100.0%; Pred. No. 0; Matches 370; Conservative 0; Mismatches
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EQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 42
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APPLICANT: Hart, Charles E.
APPLICANT: Hart, Christopher S.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVI
FILLS REFERENCE: 98-60
CURRENT APPLICATION NUMBER: US/10/139,583
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 09/457,066
PRIOR APPLICATION NUMBER: 09/457,066
PRIOR APPLICATION NUMBER: 09/457,066
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOPTWARE: FASTSEQ for Windows Version 3.0
1.ENGTH: 370
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US-10-139-583-37
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Best Local
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Local Similarity 100.0%;
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No. US20020177193A1
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APPLICANT: HART, Charles E.
APPLICANT: HART, Charles E.
APPLICANT: TOPOUZÍS, STAVEOS
TITLE OF INVENTION: COMPOSITIONS AND METHODS F
TITLE OF INVENTION: KIDNEY FUNCTION
FILE REFERENCE: 00-100
CURRENT APPLICATION NUMBER: US/10/039,847A
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: US 60/244,479
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASUSEQ FOR WINDOWS Version 3.0
SEQ ID NO 2
LENGTH: 370
TYPE: PAT
ORGANISM: Homo sapiens
US-10-039-847A-2
 Sequence 8, Application US/10260539
Publication No. US20030073637A1
GENERAL INFORMATION:
APPLICANT: EXIKSSON, Ulf
APPLICANT: AASE, Karin
APPLICANT: LI, Xuri
APPLICANT: DONTEN, Annica
APPLICANT: UUTELA, Marko
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US-10-260-539-8
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US-10-039-847A-2
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US-10-264-361-5
; Sequence 5, Application US/10264361
; Publication No. US20030087870A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATI
; FILE REFERENCE: 00-53
; CURRENT APPLICATION NUMBER: US/10/26
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; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
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PRIOR APPLICATION NUMBER: US 60/107,852
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 60/107,852
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: US 60/150,604
PRIOR FILING DATE: 1999-08-26
PRIOR FILING DATE: 1999-08-26
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 60/157,108
PRIOR APPLICATION NUMBER: US 60/157,756
PRIOR APPLICATION NUMBER: US 60/157,756
PRIOR APPLICATION NUMBER: US 09/438,046
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 2000-10-19
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.1
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Matches 370
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APPLICANT: OESTMAN, Arne
APPLICANT: HELDIN, Carl-Henrik
TITLE OF INVENTION: PLATELET DERIVED GROWTH
FILE REFERENCE: 1064/4483302
CURRENT APPLICATION NUMBER: US/10/260,539
CURRENT FILING DATE: 2002-10-01
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Local Similarity 100.0%; Pred. No. 0;
1es 370; Conservative 0; Mismatches
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         NUMBER: US/10/264,361
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APPLICANT: Su, Eric
APPLICANT: Witcher, Derrick
FILE REFERENCE: X.14392M
CURRENT APPLICATION NUMBER: US/10/258,557
CURRENT FILING DATE: 2002-10-23
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 370
TYPE: PRT
US-10-258-557-2
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PRIOR APPLICATION NUMBER: US/09/695,121;
PRIOR FILING DATE: 2000-10-23;
NUMBER OF SEQ ID NOS: 18;
SOFTWARE: FastSEQ for Windows Version 3.0;
SEQ ID NO 5;
SEQ ID NO 5;
LENGTH: 370;
TYPE: PRT;
ORGANISM: Homo sapiens
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APPLICANT: Gliberteson, Debra G.
APPLICANT: Gliberteson, Debra G.
APPLICANT: Hart, Charles E.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
FILE REFERENCE: 00-28
CURRENT APPLICATION NUMBER: US/10/226,559
CURRENT FILING DATE: 2002-08-23
PRIOR APPLICATION NUMBER: US/09/540,224
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
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                                                TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMY
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Conservative 0;
                                                                                                                                                                                                                                                                               Score 370;
Pred. No. 0;
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Disease Using Growth

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Sequence 2, Application US/10274638
Publication No. US20030109000A1
GENERAL INFORMATIQN:
APPLICANT: MOOTE, MATGATE D.
APPLICANT: MOOTE, MATGATE D.
TITLE OF INVENTION: DIMERIZED GROWTH FACTOR:
TITLE OF INVENTION: AND METHODS FOR PRODUCIL
FILE REFERENCE: 01-30
CURRENT APPLICATION UNMER: US/10/274,638
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 60/346,117
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 14
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 370
Type: PRT
ORGANISM: Homo sapiens
US-10-274-638-2
 RESULT 14
US-10-011-364-4
US-10-011-364-4
; Sequence 4, Apj
; Publication No
; GENERAL INFORM
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 Sequence 4, Application US/10011364
Publication No. US20030153495A1
GENERAL INFORMATION:
APPLICANT: Lichenstein, Henry
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APPLICANT: Shimkets, Juliette
APPLICANT: Lancochelle, William
TITLE OF INVENTION: Treatment of Inflammatory Bowel Dis
TITLE OF INVENTION: Factors
FILE REFERENCE: 19566-557A IBD CIP
CURRENT APPLICATION NUMBER: US/10/011,364
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/246,206
PRIOR APPLICATION NUMBER: 60/246,206
PRIOR APPLICATION NUMBER: 60/992,840
PRIOR FILING DATE: 2000-11-06
PRIOR FILING DATE: 2001-11-06
PRIOR FILING DATE: 2001-11-06
PRIOR FILING DATE: 2001-11-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
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LENGTH: 370
TYPE: PRT
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APPLICANT: Rosen et al.
TITLE OF INVENTION: 17
FILE REPERENCE: PS723P1
CURRENT APPLICATION NUMBER: US/10/277,802
CURRENT FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: 09/915,582
PRIOR APPLICATION NUMBER: PCT/US01/01431
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Burgess, Catherine
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Boldog, Ferenc
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Prayaga, Sudhirdas
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Length Indels

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PRIOR FILING DATE: 2001-01-1/
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR APPLICATION NUMBER: 60/281,968
PRIOR FILING DATE: 2000-09-12
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 56
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Delfani, Kioumars
APPLICANT: Janson, Ann Marie
APPLICANT: Kuhn, Georg
APPLICANT: Kuhn, Georg
APPLICANT: Plate, Karlheinz
APPLICANT: Schnazer, Anne
APPLICANT: Wachs, Frank-Peter
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Matches 370
SOFTWARE: PatentIn Ver.
SEQ ID NO 8
LENGTH: 370
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                                                CURRENT APPLICATION NUMBER: US/10/246,091
CURRENT FILLING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/323,381
PRIOR FILING DATE: 2001-09-19
PRIOR PILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/326,044
PRIOR FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                        APPLICANT: Wachs, Frank-Peter
APPLICANT: Zhao, Ming
TITLE OF INVENTION: Treatment of Central Nervous
FILB REFERENCE: 21882-504 (PDGF/VEGF)
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Wachs, Frank-Peter
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APPLICANT: FOX, Brian A.
APPLICANT: MOORE, Margaret D.
APPLICANT: Swiderek, Kristine M.
APPLICANT: Swiderek, Kristine M.
APPLICANT: Birks, Carl W.
TITLE OF INVENTION: MATERIALS AND METHODS FO.
FILE REFERENCE: 01-33
CURRENT APPLICATION NUMBER: US/10/365,095
CURRENT FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: 60/355,882
PRIOR FILING DATE: 2002-02-11
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 370
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; TYPE: PRT
; ORGANISM: Homo s
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Best Local
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Best Local Similarity
Matches 370; Conserv
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APPLICANT: Boldog, Ferenc L.
APPLICANT: Boldog, Catherine E.
APPLICANT: Burgess, Catherine E.
APPLICANT: Jeffers, Elma
APPLICANT: LaRochelle, william J.
APPLICANT: LaRochelle, william J.
APPLICANT: Lichenstein, Henry S.
APPLICANT: Prayaga, Sudhirdas
APPLICANT: Prayaga, Sudhirdas
APPLICANT: Shinkets, Juliette
APPLICANT: Shinkets, Michard A.
APPLICANT: Vang, Meijia
APPLICANT: Vang, Meijia
APPLICANT: Curagen Corporation
TITLE OF INVENTION: Treatment of Inflammatory Bowel Disease
TITLE OF INVENTION: Using Growth Factors
FILE REFERENCE: 15966-557A IBD CIP2
CURRENT APPLICATION NUMBER: US/10/321,962
CURRENT PILIG DATE: 2002-12-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: CuraBeqList version 0.1
SEQ ID NO 4
LENGTH: 370
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                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 370; Conserv
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ORGANISM: Homo sapiens
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 LDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQ
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ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-606-055-2
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CURRENT FILING DATE: 2003-06-25
PRIOR APPLICATION NUMBER: US/09/808,972
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US 60/235,295
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/564,595
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/132,250
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 13
SOFTMARE: FastSEQ for Windows Version 3.0
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US-10-606-055-2
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LENGTH: 370
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Publication No. US20040043027A1
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
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APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: 00-79
FILE REFERENCE: 00-79
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DCICSSRPPR
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APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BON
TITLE OF INVENTION: LIGAMENT AND CARTILAGE
FILE REFERENCE: 00-12
CURRENT APPLICATION NUMBER: US/10/664,432
CURRENT FILLING DATE: 2003-09-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-10-664-432-5
Sequence 2, Application US/10650284

Publication No. US20040110683A1

GENERAL INFORMATION:

APPLICANT: Hui, Rutai

APPLICANT: Chen, Jingzhou

APPLICANT: Liu, Baohua

APPLICANT: Liu, Yuquing

TITLE OF INVENTION: Cell Proliferation Factor Fwa

FILE REFERENCE: 043774/268352

CURRENT APPLICATION NUMBER: US/10/650,284

CURRENT FILING DATE: 2003-08-28

PRIOR APPLICATION NUMBER: CN01109260.2

PRIOR AFFLICATION NUMBER: CN01109260.2

PRIOR AFFLICATION NUMBER: CN01109260.2

PRIOR AFFLICATION NUMBER: CN01109260.2

PRIOR AFFLICATION NUMBER: CN01109260.2

PRIOR FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSEQ for Windows Version 4.0
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; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo s
US-10-650-284-2
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; SEQ ID NO 5
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-432-5
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APPLICANT: Hart, Charles E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHODS FOR PROMOTING GF
TITLE OF INVENTION: LIGAMENT AND CARTILAGE
FILE REFERENCE: 00-12
                                                                                                                                                                             Query Match 100.0%; S
Best Local Similarity 100.0%; S
Matches 370; Conservative 0;
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Best Local Similarity
Matches 370; Conserv
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CURRENT FILING DATE: 2003-09-19
NUMBER OF SEQ ID NOS: 5
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Pred. No. 0;
0; Mismatches
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Pred. No. 0;
0; Mismatches
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APPLICANT: Glibert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US/09/876,813
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
LENGTH: 370
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US-10-877-623-2
Gequence 2, Ar
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; TYPE: PRT
; ORGANISM: Homp sapiens
US-10-877-623-2
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Best Local Similarity
Matches 370; Conserv
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CURRENT FILING DATE: 2004-02-04
PRIOR APPLICATION NUMBER: US 60/445,021
PRIOR FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: US 60/471,412
PRIOR FILING DATE: 2003-05-16
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN VERSION 3.2
SOFTWARE: PATENTIN VERSION 3.2
TYPE: PRT
RESULT 25
(WS-10-910-938-2
(Sequence 2, Application US/10910938
Publication No. US20050031694A1
(GENERAL INFORMATION:
APPLICANT: Gilbertson, Debra G.
APPLICANT: Hart, Charles E.
(TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
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US-10-772-927A-9
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Matches 370
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TITLE OF INVENTION: VEGF-B AND PDGF MODULATION
FILE REFERENCE: 28967/39140B
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Local Similarity 100.0%; Pred. No. 0;
nes 370; Conservative 0; Mismatches
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FILE REFERENCE: 00-28
CURRENT ETILING DATE: 2004-08-03
PRIOR APPLICATION NUMBER: US/10/226,559
PRIOR FILING DATE: 2002-08-23
PRIOR APPLICATION NUMBER: US/09/540,224
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR RILING DATE: 2000-02-04
NUMBER: DATE: 2000-02-04
NUMBER: PRIOR FILING DATE: 2000-02-04
NUMBER: PRIOR FILING DATE: 2000-02-04
NUMBER: PRIOR FILING DATE: 2000-02-04
NUMBER: OF SEQ ID NOS: 9
SOFTWARE: FRSTSEQ for Windows Version 3.0
EEQ ID NO 2
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-10-910-938-2
Search completed: November 10, Job time : 167 secs
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                                                                                                                    RCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTWALVDIQLDHHERC
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2: pir2:*
3: pir3:*
4: pir4:*
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malate dehydrogena hypothetical prote hypothetical integ integrin beta 2 ch hypothetical prote phosphorylase kina phosphorylase kina hypothetical prote 5-methyltetrahydro

zinc metalloprotei phytroene dehydroge hypothetical prote chaperonin 60 alph 2-isopropylmalate probable membrane

F20D23.26 protein
E2 protein - human
bacillolysin-like
bacillolysin-like

hypothetical prote hypothetical 43.8K probable transport probable transport heat shock protein

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melanoma antigen-s ribosomal protein hypothetical prote hypothetical prote hypothetical prote endopeptidase (EC

hypothetical prote sodium channel pro laminin alpha-1 ch

myosin V

- fruit

hypothetical prote nuclear protein ST

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RESULT 2
JC7592
JC7592
spinal cord-derived growth factor-B precursor - rat
spinal cord-derived growth factor-B precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-C;Accession: JC7592
R;Hamada, T.; Ui-Tei, K.; Imaki, J.; Miyata, Y.
Biochem. Biophys. Res. Commun. 280, 733-737, 2001
A;Title: Molecular cloning of SCDGF-B, a novel growth factor homolog
A;Reference number: JC7591; MUID:21092670; PMID:11162582
A;Contents: Fetal brain
A;Contents: Fetal brain
A;Accession: JC7592
A;Molecule type: mRNA
A;Residues: 1-370 <HAM>
A;Residues: 1-370 <HAMA
A;Residues: 
A;Cross-references: UNIPROT:Q9EQT1;
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F;18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>
F;52-170/Region: CUB domain #status predicted
F;272-370/Region: homologous to platelet-derived growth factor/vascular endothelial
F;294-308/Region: conserved motif #status predicted
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Biochem. Biophys. Res. Commun. 280, 733-737, 2001
Biothem. Molecular cloning of SCDGF-B, a novel growth factor
A;Reference number: JC7591; MUID:21092670; PMID:11162582
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A; Residues: 1-370 < HAM>
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C;Date: 30-Jun-2001 #sequence
C;Accession: JC7591
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99.7%;
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Pred. No. 1.6e-275;
            DDBJ:AB052170
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RESULT S52636

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Biochem. Biophys. Res. Commun. 308, 126-132, 2003
A;Title: A novel murine PDGF-D splicing variant results in (A;Reference number: JC7998; PMID:12890490
A;Accession: JC7998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: scdgf-B
A;Gene: scdgf-B
F;1-17/Domain: secretory signal sequence #status predicted <SI
F;18-370/Product: spinal cord-derived growth factor-B #status
F;52-170/Region: CUB domain #status predicted
F;52-370/Region: homologous to platelet-derived growth factor
F;272-370/Region: conserved motif #status predicted
                                                                                                                                                                                                                                                                                                                                                        RESULT 4
S37239
                                                                                                                                                                                                                                                                                     metallothionein-like protein - white C;Species: Trifolium repens (white C;Date: 06-Jan-1995 #sequence_revis C;Accession: S37239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        platelet-derived growth factor-D - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Nov-2003 #sequence_revision 10-Nov-2003 #text_change
                                                                                                                            A; Cross-references: UNIPROT: P43398; C; Superfamily: metallothionein
                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-77 <ELL>
                                                                                                                                                                                                       A; Reference number: S37239
A; Accession: S37239
                                                                                                                                                                                                                                       submitted to the EMBL Data Library, A;Description: Sequence analysis of
                                                                                                                                                                                                                                                                       C;Accession: S3
R;Ellison, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Introns: 42/2; 110/
C; Keywords: fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: pdgf-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-370 < ZHU>
C; Comment: This protein
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Best Local S
Matches 32
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Best Local
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Best Local 9
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les 27; Conserv
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nes 32; Conserv
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4
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8; Conserv
CGGNCGCG 11
                               CGGNCGCG
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                                                              Conservative
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m repens (white clover)
#sequence_revision 06-Jan-1995
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                                                            Score 8; DB 2
Pred. No. 1.5
0; Mismatches
                                                                                                                                           EMBL: Z26492;
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two cDNA clones
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5e-20;
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                                                                                                                                         NID: g403326;
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                                                               0;
                                                                                          Length 77;
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C;Species: Orza sativa (rice)
C;Species: Orza sativa (rice)
C;Charce: 26-Feb-1999 #sequence_revision
C;Accession: T02063
R;Lee, M.C.; Kim, C.S.; Eun, M.Y.
submitted to the EMBL Data Library, Au, Description: Characterization of met.
A;Reference number: Z14532
A;Recession: T02063
A;Status: preliminary; translated from
A;Molecule type: mRNA
A;Residues: 1-80 <a href="Library">LEE</a>
A;Residues: 1-80 <a href="Library">LEE</a>
A;Residues: 1-80 <a href="Library">LEE</a>
A;Residues: Strain Milyang
C;Superfamily: metallothionein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant Cell Physiol. 32, 913-916, 1991
A;Title: Isolation of a gene for a metallothionein-like protein A;Reference number: JQ2128
A;Accession: JQ2128
A;Molecula "..."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q7M213
A;Experimental source: seedling, cv.
C;Comment: This protein participates
C;Superfamily: metallothionein
C;Keywords: metal binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metallothionein - soybean
C;Species: Glycine max (soybean)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: JQ2128
C;Accession: JQ2128
R;Kawashima_ I.; Inokuchi, Y.; Chino, M.; Kimura, M.; Shimizu, N.
                                                                                                                                                                                                                                                                   metallothionein-like protein - rice
C;Species: Oryza sațiva (rice)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
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A; Residues: 1-77 < FOL>
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A; Residues: 1-79 <KAW>
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;Species: Vicia faba (fava bean)
;Date: 14-Jul-1995 #sequence_revision
                                                                                        Cross-references: UNIPROT:022488; EMBL:AF017365; NID:g2407284; Experimental source: strain Milyang 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
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       Similarity 100.
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              CGGNCGCG 309
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                                                                        source: strain Milyang metallothionein
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0; Mismatches
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       Score 8; DB 2;
Pred. No. 1.5;
0; Mismatches
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                                                                                                                                                           from GB/EMBL/DDBJ
                                                                                                                                                                                                          , August 1997
metallothionein-like
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R;Kim, H.U.; Kim, J.B.; Yun, C.H.; I
Plant Physiol. 108, 863, 1995
A;Title: Nucleotide sequence of cDN:
A;Reference number: Z18022; MUID:95;
A;Accession: T14187
A;Accession: T14187
A;Stacus: preliminary; translated f:
A;Molecule type: mRNA
A;Residues: 1-80 <KIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metallothionein-like protein - rice
(;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_chang
C;Accession: T03404
R;Yu, L.H.; Umeda, M.; Liu, J.Y.; Zhao, N.M.; Uchimiya, H.
Gene 206, 29-35, 1998
A;Title: A novel MT gene of rice plants is strongly expressed
A;Reference number: Z14935; MUJD:98121309; PMID:9461411
A;Accession: T03404
                                                                                                                                                                                                           RESULT
T14387
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R;Michalowski, C.B.; Bohnert, H.J.
submitted to the EMBL Data Library, July
A;Description: A metallothionein homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         metallothionein - common ice plant
C;Species: Mesembryanthemum crystallinum (common ice plant)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change
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T03404
                                                                                                                                       metallothionein-like protein - turnip
C;Species: Brassica rapa (turnip)
C;Date: 20-Sep-199 #sequence_revisio:
C;Accession: T14387
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A; Accession: T12326
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A; Residues: 1-80 < YUL>
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Best Local Similarity
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                                                                    sequence of cDNA clone Z18022; MUID:95334519;
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                                                                                                                      C.H.; Kang, S.K.; Chung,
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PMID:7610190
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RESULT 11
T10087
                                 C;Genetics:
A;Introns: 22/2
C;Superfamily: metallothionein
C;Keywords: metal binding
                                                                                                                                                             submitted to the EMBL Data Library, July 1992 A;Reference number: S57897 A;Accession: S57897
                                                                                                                                                                                                                                                                                                                                                                                            metallothionein-like protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Ricinus communis (castor bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10087
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A;Experimental source: subspecies pekinensis; flower
C:Function:
                                                                                                          A; Cross-references:
                                                                                                                           A; Molecule type: DNA
A; Residues: 1-81 < TAW>
                                                                                                                                                                                                                   R; Takahashi, K.
                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P25860; EMA;Experimental source: strain Columbia
                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-81 < TAK>
                                                                                                                                                                                                                                                                                                          A; Reference number: $18069
A; Accession: $18069
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C;Keywords: metal binding
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Plant Physiol. 109, 721, 1995
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                                                                                                                                                                                                                                                                                                                                                                               C; Accession: S18069; S57897
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8; Conserv
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    castor bean

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ilarity 100.0%;
Conservative
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 2.2%;
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metallothionein type II B - tomato (;Species: Lycopersicon esculentum (tomato) C;Date: 30-Apr-1999 #sequence_revision 30-A C;Accession: T07076 R;Whitelaw, C.A.; LeHuquet, J.A.; Thurman,
                                                                                               RESULT 15
T07076
                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: Z15923; MUID:98349862; PMID:9687073
A;Stature. Terminal A;Stature. Terminal A;Accession: T07114
A;Stature. Terminal A;Accession: T07114
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$57861
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C; Superfamily: metallothionein
C; Keywords: metal binding
                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q40158; EMBL:Z68138; NID:g1103688; PIDN:CAA92243.1; PID:g110 A;Experimental source: cultivar Bonner Best; root C;Superimently: metallothionein C;Keywords: metal binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Lycopersicon esculentum (tomato)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Gen. Genet. 248, 318-328, 1995
A; Title: Structure, organization and expression of the
A; Reference number: S57858; MUID:96004699; PMID:7565594
 submitted to the
                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-82 <GIR>
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A;Residues: 1-81 <ZHO>
A;Cross-references: UNIPROT:P25860
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uquet, J.A.; Thurman, D.A.; Tomsett, A.B
Data Library, July 1996
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A;Description: The isolation and chars A;Reference number: Z15900
A;Acqession: T07076
A;Status: preliminary; translated from A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-82 <MHI>
A;Cross-references: UNIPROT:Q40158; EW
A;Experimental source: strain Ailsa cr
                                                                                                                                            metallothionein-like protein - rice
(;Species: Oryza sativa (rice)
(;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #t
(;Accession: T03787
R;Lee, M.C.; Park, J.Y.; Kim, Y.H.; Eun, M.Y.
submitted to the EMBL Data Library, October 1996
A;Description: Molcular cloning and characterization
A;Reference number: Z15085
A;Accession: T03787
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C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #te
C;Accession: T03727
R;Chen, W.M.; Heich, H.M.; Huang, P.C.
submitted to the EMBL Data Library, December 1996
A;Description: Signification of two introns in type 2
A;Reference number: 215032
A;Accession: T03727
                                                                                              A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-84 <LEE>
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C; Superfamily: metallothionein
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A;Experimental source: cv. Tainung 67, root
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A; Residues: 1-82 < CHE>
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C;Species: Oryza sativa (rice)
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Query Match 2.2%; Sometime 2.2%; Sometimes Similarity 100.0%; Matches Sometime O;
                                                                Cross-references: UNIPROT:P93433; Superfamily: metallothionein
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Introns: 22/
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D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simose, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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AB1244
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Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.;
R;Glaser, P.; Frangeul, L.; Buchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; F
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                                                                                                                                          A;Gene: lin1391
C;Superfamily:
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                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-353 <GLA>
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A;Experimental source: strain EGD-e
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A; Residues: 1-353 <GLA>
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0; Mismatches
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                                                                      mismatches
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Voss, H.; Wehland,
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Fsihi, H
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Fsihi, H
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A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J. A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1398
                                                                                                                                                                                                                                                                                  C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change
C;Accession: AB1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Walsh, J.; Waters, C.A.; Freeling, M. Genes Dev. 12, 208-218, 1998
A; Title: The maize gene liguleless2 encodes A; Reference number: Z14322; MUID:98154557; FA; Accession: T01415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Zea mays
C; Date: 12-Feb-1999
C; Accession: T01415
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C;Superfamily: glucose-6-phosphate of
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - C;Species: Zymomonas mobilis C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #C;Accession: B37855
    A; Cross-references:
                        A; Molecule type: DNA
A; Residues: 1-995 <GLA>
                                                                                                                                                                                               Science 294,
                                                                                                                                                                                                                                       R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; I
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A; Residues: 1-531 <WAL>
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A;Title: Sequence and genetic organization of a Zymomonas mobilis A;Reference number: A37855; MUID:91072278; PMID:2254282
A;Accession: B37855
                                                               A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: UNIPROT: 049067; EMBL: AF036949; NID: 92865393; PIDN: AAC39351.1;
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                                                                                                                                                                                                                                                                                                                                                    formate dehydrogenase alpha chain homolog
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4, 849-852, 2
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8; Conserv
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UNIPROT: Q8Y469; GB:NC_003210; PIDN: CAD00664.1; PID: g16412074;
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Pred. No.
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dehydrogenase
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PMID:9490265
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9 2
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Voss, H.; W
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Fsihi, H.
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Wehland,
    GSPDB:
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                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-1138 < PAR>
A; Residues: 1-1138 < PAR>
A; Cross-references: EMBL:X60957
A; Cross-references: EMBL:X60957
R; Partanen, J.; Maekelae, T.P.; Alitalo, R.; Lehvaeslaiho, H.; Alitalo, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
A; Title: Putative tyrosine kinases expressed in K-562 human leukemia colls
A; Reference number: A38268; MUID:91062389; PMID:2247464
A; Accession: C38269
A; Accession: C38269
                      A;Experimental source: clone JTK14 R;Korhonen, J.; Lahtinen, I.; Halm Blood 86, 1828-1835, 1995
                                                                                                                                                                                                                                                                                                                                                                      protein-tyrosine kinase (BC 2.7.1.112), receptor type the C;Species: Homo sapiens (man) C;Date: 19-Feb-1994 #sequence revision 11-Aug-1995 #text_C;Accession: S24066; C38269; T52613 R;Partanen, J.; Armstrong, E.; Maekelae, T.P.; Korhonen, Mol. Cell. Biol. 12, 1698-1707, 1992 A;Title: A novel endothelial cell surface receptor tyros:
                                                                                     A; Molecule type: mRNA
A; Residues: 981-1034 < PAW>
                                                                                                                                                                                                                                                                                                                             A; Accession: S24066
                                                                                                                                                                                                                                                                                                                                               A; Title: A novel endothelial cell surface : A; Reference number: $24066; MUID: 92195316;
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(EC 2.7.1.112), receptor type tie precursor -

human

#text_change

J.; Sandberg, M.; Renkonen, R.;

with extracellular

receptor tyrosine kinase; PMID:1312667

Endothelial-specific gene

expression directed

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Halmekyto,

M.; Alhonen,

L.; Janne, J.;

Dumont,

D.;

Alitalo

acid sequence

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shown;

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A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-lA;Title: Comparative genomics of Listeria species. A;Reference number: AB1077; MUID:21537279; PMID:11679669 A;Accession: AE1773
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
AE1773
                                                                                                                   C; Superfamily: NAD-dependent formate dehydrogenase
                                                                                                                                   A;Gene:
                                                                                                                                                               A; Cross-references: UNIPROT: Q927Q7; GB: AL592022; A; Experimental source: strain Clip11262
                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-995 < GLA>
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                                                                                                                                                                                                                                                                                                                Science 294,
                                                                                                                                                                                                                                                                                                                                                              R;Glaser,
                                                                                                                                                                                                                                                                                                                                                                          C; Accession: AE1773
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001
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Pred. No.
                                                                         Score 8;
Pred. No.
                                                         Mismatches
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                                                                DB .
14;
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                                                                                                                                                                               PIDN: CAC97957.1;
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                                                                                     Length 995;
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; Entian, K.D.; J
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                                                           Gaps
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Voss, H.; Wehland,
                                                                                                                     2[4Fe-4S]
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Fsihi, H.
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Company - Marchage or

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Query Match
Best Local Similarity
Warches 7; Conserva
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genca; Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: G90831
Search completed: November 10, 2005, 09:47:35
Job time : 43 secs
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                                                                                                                                                                                                                                                                                                               C; Superfamily: phage PA2 endopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-153 < HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable endopeptidase [imported] - Escherichia coli (strain 0157:H7, substrain RIMD C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 25
G90831
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A;Gene: GDB:TIE; JTK14
A;Cross-references: GDB:212873; OMIM:600222
A;Map position: 1p34-1p33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: G90831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP; Superfamily: protein-tyrosine kinase, receptor type tie; EGF homology; fibronectin typ; Keywords ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphorylation; duplication; glycoprotein; phosphoprotein; phosphorylation; comparing the signal sequence #status predicted <SIG>
12-1138/Product: protein-tyrosine kinase, receptor-type tie #status predicted <WAT>
36-107/Domain: EGF homology <EG1>
36-255/Domain: EGF homology <EG1>
315-255/Domain: EGF homology <EG3>
316-344/Domain: EGF homology <EG3>
316-344/Domain: immunoglobulin homology <IM2>
316-344/Domain: immunoglobulin homology <IM2>
316-330/Domain: fibronectin type III repeat homology <FN3A>
316-331/Domain: fibronectin type III repeat homology <FN3B>
316-730/Domain: fibronectin type III repeat homology <FN3B>
316-730/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                          Genetics:
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,845-853/Region: protein kinase ATP-binding motif
,43-105,372-428/Disulfide bonds: #status predicted
,83,161,503,596,709/Binding site: carbohydrate (Asn) (covalent) #status predicted
,870,887,979/Active site: Lys, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Overy Match
Best Local Similarity
Matches 8; Conserv
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;Residues: 1-19 <RES>
;Cross-references: GB:S79347; NID:g1086921; PIDN:AAD14299.1; PID:g4261999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reference number: I52613; MUID:95383653; PMID:7655012; Accession: I52613
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                                                                                                                                                                                                                                  Score 7; Pred. No.
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o. 15;
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